



## Sequence Listing

<110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan l.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.

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Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195

Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys	
				200					205					210	
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala	
				215					220					225	
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu	
				230					235					240	
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser	
				245					250					255	
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His	
				260					265					270	
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys	
				275					280					285	
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala	
				290					295					300	
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn	
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Pro	Lys	Ala	Val												

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

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 gcccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200  
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala
				20					25					30

Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				35					40					45

His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr
				50					55					60

Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp
				65					70					75

Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu
				80					85					90

Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala
				95					100					105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			



395					400					405				
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
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His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
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<212> DNA  
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<220>  
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<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-44  
<223> Synthetic construct.

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<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgtg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300  
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 cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400  
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<210> 17  
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 <212> PRT  
 <213> Homo sapiens  
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<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

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                   20                  25                  30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
                   35                  40                  45  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
                   50                  55                  60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
                   65                  70                  75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
                   80                  85                  90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
                   95                  100                  105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
                   110                  115                  120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
                   125                  130                  135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp	
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala	
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His	
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His	
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly	
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu	
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe	
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg	
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly	
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu	
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp	
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Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
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<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
 <223> Synthetic construct  
  
 <400> 19  
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 <210> 20  
 <211> 46  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-46  
 <223> Synthetic construct.  
  
 <400> 20  
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 <210> 21  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens  
  
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 gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150  
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 <213> Homo sapiens  
  
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 <221> sig\_peptide  
 <222> 1-15  
 <223> Signal peptide.  
  
 <220>  
 <221> misc\_feature  
 <222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
          20             25             30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
          35             40             45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
          50             55             60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
          65             70
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgctc ccccgaggc 200
cccgcccgc agcatggagc caccggagc ccggcggggc cgcgcgagc 250
cgccgtgtt gctgccgctc tcgctgttag cgctgctgc gctgctggga 300
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tgggcggccc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagg tcctgcccgc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
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 <212> PRT  
 <213> Homo sapiens

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 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

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 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn Lys Ile Ser	Glu Leu Lys Asn Gly Ser	Phe Ser Gly Leu Ser
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Leu Leu Glu Arg	Leu Asp Leu Arg Asn Asn	Leu Ile Ser Ser Ile
	110	115 120
Asp Pro Gly Ala	Phe Trp Gly Leu Ser Ser	Leu Lys Arg Leu Asp
	125	130 135
Leu Thr Asn Asn	Arg Ile Gly Cys Leu Asn	Ala Asp Ile Phe Arg
	140	145 150
Gly Leu Thr Asn	Leu Val Arg Leu Asn	Leu Ser Gly Asn Leu Phe
	155	160 165
Ser Ser Leu Ser	Gln Gly Thr Phe Asp Tyr	Leu Ala Ser Leu Arg
	170	175 180
Ser Leu Glu Phe	Gln Thr Glu Tyr Leu Leu	Cys Asp Cys Asn Ile
	185	190 195
Leu Trp Met His	Arg Trp Val Lys Glu Lys	Asn Ile Thr Val Arg
	200	205 210
Asp Thr Arg Cys	Val Tyr Pro Lys Ser Leu	Gln Ala Gln Pro Val
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Thr Gly Val Lys	Gln Glu Leu Leu Thr Cys	Asp Pro Pro Leu Glu
	230	235 240
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Glu Gly Asp Ser	Leu Pro Phe Gln Cys Met	Ala Ser Tyr Ile Asp
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Gln Asp Met Gln	Val Leu Trp Tyr Gln Asp	Gly Arg Ile Val Glu
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Thr Asp Glu Ser	Gln Gly Ile Phe Val Glu	Lys Asn Met Ile His
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	305	310 315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys His	Val Gln Thr Lys Arg
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Gly Asn Asn Thr	Arg Thr Val Asp Ile Val	Val Leu Glu Ser Ser
	335	340 345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val Val	Asn Asn Lys Gly Asp
	350	355 360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly Ile	Thr Ala Tyr Leu Gln
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Cys Thr Arg Asn	Thr His Gly Ser Gly Ile	Tyr Pro Gly Asn Pro

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Trp	Ala	Asp	Asp	Asp	Tyr	Ser	Arg	Cys	Gln	Tyr	Ala	Asn	Asp	Val					
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Thr	Arg	Val	Leu	Tyr	Met	Phe	Asn	Gln	Met	Pro	Leu	Asn	Leu	Thr					
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Asn	Ala	Val	Ala	Thr	Ala	Arg	Gln	Leu	Leu	Ala	Tyr	Thr	Val	Glu					
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Met	Ile	Glu	Lys	Phe	Gly	Arg	Phe	Thr	Lys	Glu	Glu	Lys	Ser	Lys					
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Glu	Leu	Gly	Asp	Val	Met	Val	Asp	Ile	Ala	Ser	Asn	Ile	Met	Leu					
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Cys	Ser	Arg	Ile	Val	Gln	Cys	Leu	Gln	Arg	Ile	Ala	Thr	Tyr	Arg					
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Leu	Ala	Gly	Gly	Ala	His	Val	Tyr	Ser	Thr	Tyr	Ser	Pro	Asn	Ile					
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Ala	Leu	Glu	Ala	Tyr	Val	Ile	Lys	Ser	Thr	Gly	Phe	Thr	Gly	Met					
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Thr	Cys	Thr	Val	Phe	Gln	Lys	Val	Ala	Ala	Ser	Asp	Arg	Thr	Gly					
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Leu	Ser	Asp	Tyr	Gly	Arg	Arg	Asp	Pro	Glu	Gly	Asn	Leu	Asp	Lys					
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Gln	Leu	Ser	Phe	Lys	Cys	Asn	Val	Ser	Asn	Thr	Phe	Ser	Ser	Leu					
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 <212> DNA  
 <213> Artificial

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 <222> 1-24

<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<210> 27

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<212> DNA

<213> Artificial

<220>

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<222> 1-50

<223> Synthetic construct.

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaatcggga 150

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                     20                    25                    30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
                     35                    40                    45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
                     50                    55                    60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
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 Lys Gly Ser Gln Lys Ser  
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 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

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 <211> 322  
 <212> PRT  
 <213> Homo sapiens

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 50 55 60  
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
 80 85 90  
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105  
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
 110 115 120  
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
 125 130 135  
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
 140 145 150  
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
 200 205 210

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Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
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Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
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Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
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Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
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 <212> DNA  
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 ggatcttctc ttctctgga ggctttggaa tgatgaaagc atgtaccctc 3050  
 cacccttttc ctggccccct aatggggcct gggccctttc ccaaccctc 3100  
 ctaggatgtg cgggcagtgt gctggcgct caccagcagc cgggctgccc 3150  
 attcacgcag agctctctga gcgggagggt gaagaaagga tggctctggt 3200  
 tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250  
 cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaggaat 3300  
 tgtgccagt agtgacagtc atgaggagt gtctcttctt ggggaggaaa 3350  
 gaaggtagag ctttctgtc tgaatgaaag gccaaaggta cagtacaggg 3400  
 cccgccccca gccagggtgt taatgccac gtagtggagg cctctggcag 3450  
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 ggtgggtggc' tttagaatta agggccttgt aggctttggc aggtaagagg 3550  
 gcccaaggta agaacgagag ccaacgggca caagcattct atatataagt 3600

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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala	Ser	Gln	Leu	Leu	Gly	Asp	Glu	Leu	Leu	Leu	Ala	Lys	Leu	Pro
			245						250					255
Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
			320						325					330
Glu	Pro	Glu	Glu	Gln										
			335											

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
 tgtcctttgt cccagacttc tgtcc 25

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
 ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 37  
ggcgagccct aactatccag gag 23

<210> 38  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-39  
<223> Synthetic construct.

<400> 38  
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 39  
ctgctgcaaa gcgagcctct tg 22

<210> 40  
<211> 2084  
<212> DNA  
<213> Homo sapiens

<400> 40  
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ttttgtttcc ctggcaccct cctgctcagt gcgacattgt cactttaac 100  
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200  
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
caatctattc ttgccacatc aagggtattgt tattccttta aaaaaaac 300

aataccaaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350  
caacgttggt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400  
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaatctc aaggcgagtc attcccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattctttg ggcagtctaa aaccacatc taccatttcc acaagccctc 650  
ccttgatcca tagctttggt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgccat ctccagcat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtctttggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850  
ccatctgtga ccccttgat agtgaacca agtgatggc ttaccacaaa 900  
cagtgatagc ttactgggt ttaccctta tcaagaaaaa acaactctac 950  
agcctacctt aaaattcacc aataattcaa aactctttcc aaatacgtca 1000  
gatcccaaaa aagaaaatag aaatacagga atagtattcg gggccatttt 1050  
aggtgctatt ctgggtgtct cattgcttac tcttggtggc tacttgttgt 1100  
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agaaatgaac cagttctgcg attagacaat gcaccggaac cttatgatgt 1200  
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250  
tgccagaaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300  
cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350  
gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400  
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450  
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tttcttaciaa tttttggcca tcctgaggca ttactaagt agccttaatt 1550  
tgtattttag tagtattttc ttagtagaaa atatttgtgg aatcagataa 1600  
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650  
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700  
tgccatgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750

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catagcccag agtttctggt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900  
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000  
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr 15  
1 5 10  
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn 30  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys 45  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu 60  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu 75  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn 90  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr 105  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val 120  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser 135  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr 150  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser 165  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val 180  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser 195  
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 aacaggatct cctcttgacg tctgcagccc aggacgctga ttccagcagc 50  
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100  
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaagt ggaggccctc 150  
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
 tgccaccagc gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350  
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400  
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550



ggaactgcta tctgatgccc ctcaatactt ctattgttat gcttccaaaa 600  
 aatctggttag agctcttttg caaactggcg agtggcagat atctgcctca 650  
 aacttatgtg gttcgagaag acctagtgtc tgtggaggaa attcgtgatg 700  
 ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750  
 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800  
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
 agaagtca gatttacaat atgacttta cattaagggt tatgggatac 950  
 tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000  
 gaaaaaaaa aaaactacta accactgcaa gctcttgtca aattttagtt 1050  
 taattggcat tgcttgtttt ttgaaactga aattacatga gtttcatttt 1100  
 ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200  
 tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250  
 tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300  
 tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350  
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450  
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500  
 tgtgtagggt ctgaatgctg taaggagttt aggttgatg aattctacaa 1550  
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
 <211> 263  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu  
 1 5 10 15  
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg  
 20 25 30  
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
 35 40 45  
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaactgct atctgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttgcatgc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgaac cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggaggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100  
 cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
 gtttcggcgg cagccccag cctcctcatc cttctgttgc tgetgctggg 200  
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250  
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 ccgagcctcc cgccaccctg gaccccgcc ctcagcccca catcgatggg 350  
 gccccagccc acaaccttg ggggcccatc acccccacc aacttcctgg 400  
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450  
 ggctccctgg cctttctgct gatgttcac gtctgtgccg cggtcatcac 500  
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc tccccaaaga 550  
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600  
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
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 cccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
 ggcaggggcg cagaggaaga ggagaaggc agccaggagg gggaccagga 800  
 • agtcaggga catgggtcc cagtggagac accagaggcg caggaggagc 850  
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900  
 gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950  
 tcccccgaa agccctgtg cttgcagcag tgtccacccc agtgtctaac 1000  
 agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050  
 ccccggtgat gaaaaggcct tcagccctga ctgttcctg acactccctc 1100  
 cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150  
 cagaaatgct ggtccccggt gcccggagg aatcttacca agtgccatca 1200  
 tccttcacct cagcagcccc aaagggtac atcctacagc acagctccc 1250  
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350  
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
 aatactgctc ttaattttcc tgaagggtgc cccctgtttc tagttggtcc 1450  
 aggattaggg atgtgggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
 gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600  
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650  
 ggggctgggg aagggtttct gacgccagc ctggagcagg ggggccctgg 1700  
 ccacccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
 gtcagtcctc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800  
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1950  
 aaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu  
 20 25 30  
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
 80 85 90  
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
 95 100 105  
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
 110 115 120  
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
 125 130 135  
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
 140 145 150  
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
 155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr  
 170 175 180  
 Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp  
 185 190 195  
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 Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro  
 215 220 225  
 Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu  
 230 235 240  
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly  
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<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

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Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

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Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Asn	Gly	His				
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Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly					
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 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
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 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
 380 385 390  
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
 395 400 405  
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
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 <211> 280  
 <212> PRT  
 <213> Homo sapiens

<400> 54

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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
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Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
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Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
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Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
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Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
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Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
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Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<211> 2401  
<212> DNA  
<213> Homo sapiens

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<210> 56  
<211> 299  
<212> PRT  
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<400> 56  
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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
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Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
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 <211> 4277  
 <212> DNA  
 <213> Homo sapiens

<400> 57

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<210> 58  
 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
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Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

560										565				570			
Arg	Pro	Lys	Pro	Glu	Ile	Met	Ala	Ser	Lys	Glu	Gln	Gln	Ile	Gln			
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Arg	Asp	Asp	Pro	Gly	Ala	Ser	Pro	Gln	Ser	Ser	Ser	Gln	Pro	Asp			
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His	Gly	Arg	Leu	Ser	Pro	Pro	Glu	Ala	Pro	Asp	Arg	Pro	Thr	Ile			
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Ser	Thr	Ala	Ser	Glu	Thr	Ser	Val	Tyr	Val	Thr	Trp	Ile	Pro	Arg			
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Gly	Asn	Gly	Gly	Phe	Pro	Ile	Gln	Ser	Phe	Arg	Val	Glu	Tyr	Lys			
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Lys	Leu	Lys	Lys	Val	Gly	Asp	Trp	Ile	Leu	Ala	Thr	Ser	Ala	Ile			
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Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly			
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Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu			
				680					685					690			
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr			
				695					700					705			
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr			
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Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met			
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Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr			
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Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys			
				755					760					765			
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His			
				770					775					780			
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn			
				785					790					795			
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr			
				800					805					810			
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro			
				815					820					825			
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg			
				830					835					840			
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro			
				845					850					855			

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu		950	955	960
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His		965	970	975
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly		980	985	990
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro		995	1000	1005
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys		1010	1015	1020
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg		1025	1030	1035
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro		1040	1045	1050
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu		1055	1060	1065
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp		1070	1075	1080
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly		1085	1090	1095
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr		1100	1105	1110
Pro	Pro	Leu	Thr	Ile												1115		

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 <212> DNA  
 <213> Artificial

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 <213> Artificial  
  
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 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 60  
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 <210> 61  
 <211> 42  
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 <213> Artificial  
  
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 <222> 1-42  
 <223> Synthetic construct.  
  
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 <210> 62  
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 <400> 62  
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<210> 63  
 <211> 487  
 <212> PRT  
 <213> Homo sapiens



<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

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Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
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Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
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Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
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Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
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Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
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Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
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Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
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Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
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Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
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Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
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Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
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Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260										265					270				
Ser	Asp	Thr	Leu	Ile	Arg	Arg	Val	Leu	Glu	Val	Ser	Gln	Ala	Pro					
				275					280					285					
Val	Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Ala	Val	Cys	Asp	Asn	Leu					
				290					295					300					
Leu	Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Asn	Gly	Gly					
				305					310					315					
Ile	Val	Met	Val	Thr	Leu	Ser	Met	Gly	Val	Leu	Gln	Cys	Asn	Leu					
				320					325					330					
Leu	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Arg					
				335					340					345					
Ala	Val	Ile	Gly	Ser	Glu	Phe	Ile	Gly	Ile	Gly	Gly	Asn	Tyr	Asp					
				350					355					360					
Gly	Thr	Gly	Arg	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr					
				365					370					375					
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Xaa	Trp	Ser	Glu	Glu					
				380					385					390					
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg					
				395					400					405					
Gln	Val	Glu	Lys	Val	Arg	Glu	Glu	Ser	Arg	Ala	Gln	Ser	Pro	Val					
				410					415					420					
Glu	Ala	Glu	Phe	Pro	Tyr	Gly	Gln	Leu	Ser	Thr	Ser	Cys	His	Ser					
				425					430					435					
His	Leu	Val	Pro	Gln	Asn	Gly	His	Gln	Ala	Thr	His	Leu	Glu	Val					
				440					445					450					
Thr	Lys	Gln	Pro	Thr	Asn	Arg	Val	Pro	Trp	Arg	Ser	Ser	Asn	Ala					
				455					460					465					
Ser	Pro	Tyr	Leu	Val	Pro	Gly	Leu	Val	Ala	Ala	Ala	Thr	Ile	Pro					
				470					475					480					
Thr	Phe	Thr	Gln	Trp	Leu	Cys													
				485															

<210> 64  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 65  
 gtcacacaca gctctggcag ctgag 25

<210> 66  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 66  
 ,ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67  
 <211> 1564  
 <212> DNA  
 <213> Homo sapiens

<400> 67  
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 aacaccacaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100  
 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150  
 cggtgttttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200  
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250  
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300  
 gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgctg 350  
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggc catcattgtc 400  
 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450  
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650  
 atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
 ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
 aagagggatg tggctctctga tctctgttgt cttcttggtt ctttgggggt 900  
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
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 cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050  
 ttcaggaact cagtgtctgg gaggaaagca tggcccagca ttcagcatgt 1100  
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 ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200  
 tgggccccct gagccactg ggtcttcagg gtgcactgga agctggtgtt 1250  
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300  
 ctctgtctgc ggtccctca cctgcacttg aggggtcttg gcagtccctc 1350  
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
 gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450  
 gcctcttgtc cctgaacttc gttgtaccag tgcattgaga gaaaattttg 1500  
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 ttttatttct ctca 1564

<210> 68

<211> 183

<212> PRT

<213> Homo sapiens

<400> 68

Met	Lys	Leu	Leu	Ser	Leu	Val	Ala	Val	Val	Gly	Cys	Leu	Leu	Val
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Pro	Pro	Ala	Glu	Ala	Asn	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Cys	Lys
				20					25				30	

Cys	Ile	Cys	Pro	Pro	Tyr	Arg	Asn	Ile	Ser	Gly	His	Ile	Tyr	Asn
				35				40					45	

Gln	Asn	Val	Ser	Gln	Lys	Asp	Cys	Asn	Cys	Leu	His	Val	Val	Glu
				50				55					60	

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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 agttcatagg gtctgggtc cccgaaccag gaagggttga gggaacacaa 100  
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggcctccc 150  
 tccctttgca ttcccacccc tccgggcttt gcgtcttcct ggggaccccc 200  
 tcgcccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250  
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtc tctctgggcg gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
 gcatgtgctg ccccgatacc cgctgcaata atggcatctg tatcccagtt 600  
 actgaaagca tcttaacccc tcacatccc gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcatatatag 1050  
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350  
ttatacaaat aacctacatg ccagatttct attcaacggt agagttaac 1400  
aaaatactcc tagaataact tggtatacaa taggttctaa aaataaaatt 1450  
gctaaacaag aatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttgg 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700  
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aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatattt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150  
 tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200  
 tcagtgtgag gtctctgtgc cgtactatcc tcaaattatt tattttatag 2250  
 tgctgagatc ctcaaataat ctcaatttca ggagggttca caaatgtac 2300  
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 caaaaattat aaactagtcc atccaagaac caaagtittgt ataaacaggt 2850  
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 atataacaat tattatattt acaatttggg ttctgcaata tttttcttat 2950  
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 gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100  
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 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
 20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
 35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
                             50                            55                            60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
                             65                            70                            75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
                             80                            85                            90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
                             95                            100                            105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
                             110                            115                            120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
                             125                            130                            135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
                             140                            145                            150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
                             155                            160                            165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
                             170                            175                            180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
                             185                            190                            195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
                             200                            205                            210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
                             215                            220                            225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
                             230                            235                            240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
                             245                            250                            255  
 Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100  
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcattttatt 200



tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250  
atatttttagt aattcatatg ttttagatta taggttttaa cataacttggtg 300  
aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350  
ggatttggtc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400  
tttgagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttgaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
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agcaccagag ccaggcagtc actgttcctc ctcttggtt ggagtccttt 700  
ccttcccagg caaaacttgc agaatcaaca cctggagaca gtccctccac 750  
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tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
atacccccag cttctaagat ccagcttct gcagtggaaa tgcttggtc 900  
agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950  
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aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050  
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tttaaagatg cttgggccag gcggggtggc tgatgcccat aatcccagtg 1600  
ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
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1 5 10 15  
Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
20 25 30  
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser Ser Glu Asn	Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys	230	235	240
Ser Leu Ser Glu	Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala	245	250	255
Val Gln Asn Ser	Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser	260	265	270
Leu Thr Ser Ser	Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser	275	280	285
Ser Ser Tyr Asp	Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln	290	295	300
Ser Pro Val Ser	Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn	305	310	315
Gly His Gly Gly	Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr	320	325	330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg	335	340	345
Lys Arg Ile Ala	His Val Met Trp Lys Thr Pro Val Gly Gln Trp	350	355	360

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 74  
 tggtaaactg gcccaaactc gg 22

<210> 75  
 <211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcac ccgtccttgg ctacaggattt ggagagcttg caccaccaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
gccagtgagg acaaagcctg gggctgggag ggggcatgg cgctgccatc 50  
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200  
caccgacggc cccccggcca cccccgcta ctgggacggc gagaaggagg 250  
tgctggcggg ggcgcgcggc gcaccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350  
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tggaacctta cgcgtcgggc gagcgccgcg cctacgggcc ctttttctg 450  
cgcgaccgcg tggctgtggg cgcggatgcc tttagcgcg gtgacttctc 500  
actcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550  
acctgcacca ccattactgt ggctgcacg aacgcgcgt cttccacctg 600  
acggtcgcgc aacccacgc ggagccgcc ccccggggt ctccgggcaa 650  
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gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750  
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<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30
Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45
Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60
Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	140	145	150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	155	160	165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	170	175	180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	185	190	195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	200	205	210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	215	220	225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	230	235	240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	245	250	255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	260	265	270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	275	280	285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	290	295	300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	305	310	315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	320	325	330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys					335	340	

<210> 78  
 <211> 2243  
 <212> DNA  
 <213> Homo sapiens

<400> 78

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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
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 gccattggtt caaggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79  
 <211> 475  
 <212> PRT  
 <213> Homo sapiens

<400> 79  
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 Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala  
 20 25 30  
 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg  
 35 40 45  
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu  
 50 55 60  
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys  
 65 70 75  
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr  
 80 85 90  
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser  
 95 100 105



Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val		110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val		125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr		140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe		155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr		170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met		185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr		200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp		215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe		230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu		245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe		260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser		275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro		290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val		305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile		320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe		335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu		350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn		365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile		380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys				

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser			
	410	415		420	
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu			
	425	430		435	
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly			
	440	445		450	
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser			
	455	460		465	
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250  
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 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu  
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 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln  
                     20                    25                    30  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
                     35                    40                    45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
                     50                    55                    60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
                     65                    70                    75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
                     80                    85                    90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
                     95                    100                    105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
                     110                    115                    120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
                     125                    130                    135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
                     140                    145                    150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
                     155                    160                    165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
170	175	180	
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
185	190	195	
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200	205	210	
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215	220	225	
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230	235	240	
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245	250	255	
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260	265	270	
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275	280	285	
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290	295	300	
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305	310	315	
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320	325	330	
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335	340	345	
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350	355	360	
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365	370	375	
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380	385	390	
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395	400	405	
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410	415	420	
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425	430	435	
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440	445	450	
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

<210> 85  
 <211> 3316  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150  
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200  
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 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400  
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 tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550  
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 acgtactcta tggtagctgt acctctgtat gacaccttgg gaccagaagc 750

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agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000  
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050  
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
				20					25				30	



Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser		35	40	45
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile		50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys		65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg		80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val		95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn		110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu		125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu		140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys		155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His		170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala		185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr		200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu		215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile		230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu		245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro		260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu		275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe		290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys		305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr				

320										325					330				
His	Gln	Asn	Ile	Val	Ser	Asn	Ala	Ala	Ala	Phe	Leu	Lys	Cys	Val					
				335										345					
Glu	His	Ala	Tyr	Glu	Pro	Thr	Pro	Asp	Asp	Val	Ala	Ile	Ser	Tyr					
				350					355					360					
Leu	Pro	Leu	Ala	His	Met	Phe	Glu	Arg	Ile	Val	Gln	Ala	Val	Val					
				365					370					375					
Tyr	Ser	Cys	Gly	Ala	Arg	Val	Gly	Phe	Phe	Gln	Gly	Asp	Ile	Arg					
				380					385					390					
Leu	Leu	Ala	Asp	Asp	Met	Lys	Thr	Leu	Lys	Pro	Thr	Leu	Phe	Pro					
				395					400					405					
Ala	Val	Pro	Arg	Leu	Leu	Asn	Arg	Ile	Tyr	Asp	Lys	Val	Gln	Asn					
				410					415					420					
Glu	Ala	Lys	Thr	Pro	Leu	Lys	Lys	Phe	Leu	Leu	Lys	Leu	Ala	Val					
				425					430					435					
Ser	Ser	Lys	Phe	Lys	Glu	Leu	Gln	Lys	Gly	Ile	Ile	Arg	His	Asp					
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Ser	Phe	Trp	Asp	Lys	Leu	Ile	Phe	Ala	Lys	Ile	Gln	Asp	Ser	Leu					
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Gly	Gly	Arg	Val	Arg	Val	Ile	Val	Thr	Gly	Ala	Ala	Pro	Met	Ser					
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Thr	Ser	Val	Met	Thr	Phe	Phe	Arg	Ala	Ala	Met	Gly	Cys	Gln	Val					
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Tyr	Glu	Ala	Tyr	Gly	Gln	Thr	Glu	Cys	Thr	Gly	Gly	Cys	Thr	Phe					
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Thr	Leu	Pro	Gly	Asp	Trp	Thr	Ser	Gly	His	Val	Gly	Val	Pro	Leu					
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Ala	Cys	Asn	Tyr	Val	Lys	Leu	Glu	Asp	Val	Ala	Asp	Met	Asn	Tyr					
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Phe	Thr	Val	Asn	Asn	Glu	Gly	Glu	Val	Cys	Ile	Lys	Gly	Thr	Asn					
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Val	Phe	Lys	Gly	Tyr	Leu	Lys	Asp	Pro	Glu	Lys	Thr	Gln	Glu	Ala					
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Leu	Asp	Ser	Asp	Gly	Trp	Leu	His	Thr	Gly	Asp	Ile	Gly	Arg	Trp					
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Leu	Pro	Asn	Gly	Thr	Leu	Lys	Ile	Ile	Asp	Arg	Lys	Lys	Asn	Ile					
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Phe	Lys	Leu	Ala	Gln	Gly	Glu	Tyr	Ile	Ala	Pro	Glu	Lys	Ile	Glu					
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Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
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Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
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Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
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Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
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Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
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Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His Ile Gln Asp

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 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
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 35 40 45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
 50 55 60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
 65 70 75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
 80 85 90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
 95 100 105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
 110 115 120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

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Asp Pro Ala Leu	Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly	
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Trp Val Leu Arg	Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro	Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg	
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Met Pro Glu Gln	Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val	
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Ser Arg Ser Tyr	His Phe Gly Ile Val Gly Leu Asn Met Asn Gly	
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Tyr Phe His Glu	Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val	
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Pro Gly Val Gln	Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala	
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Tyr Glu Val Glu	Val His Arg Leu Leu Ser Glu Ala Glu Val Leu	
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Asp His Ser Lys	Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr	
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Glu Gly His Thr	Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp	
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Asp Leu Asp Val	Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe	
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Arg Lys Lys Asn	His Phe Leu Val Val Gly Val Pro Ala Ser Pro	
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Pro Pro Pro Lys	Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr	
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<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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 <211> 22  
 <212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial sequence  
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 <400> 90  
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 <212> DNA  
 <213> Artificial  
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 <212> DNA  
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 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
                     200                    205                    210  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
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 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

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Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu
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Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly
	260								265					270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg
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Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile
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<211> 401

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<213> Homo sapiens

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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
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<211> 3671

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

<400> 102

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Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	
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Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	
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Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	
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Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
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Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
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His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
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His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
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Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
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Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
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Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
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Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
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Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
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Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
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Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
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Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
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Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

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Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
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Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
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Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680	685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755	760		765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775		780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met		Gln	Glu	Glu	Phe	Arg	Gly				
				800						805					810				
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly		Pro	Leu	Thr	Val	Ala	Ala				
				815						820					825				
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala		Ala	Met	Val	Thr	Ala	Leu				
				830						835					840				
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu		Leu	His	Ala	Glu	Arg	Ile				
				845						850					855				
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu		Gln	Ser	Phe	Leu	Leu	Leu				
				860						865					870				
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val		Thr	Thr	Pro	Gly	Pro	Phe				
				875						880					885				
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala		Trp	Ala	Leu	Met	Ala	Thr				
				890						895					900				
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln		Pro	Val	Phe	Pro	Ala	Ile				
				905						910					915				
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe		Pro	Glu	Gly	His	Gly	Ser				
				920						925					930				
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val		Gly	Ala	Asn	Thr	Phe	Ala				
				935						940					945				
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys		Pro	Leu	Leu	Leu	Leu	Trp				
				950						955					960				
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu		Arg	Lys	Arg	Gln	Gln	Pro				
				965						970					975				
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val		Arg	Pro	Glu	Glu	Glu	Glu				
				980						985					990				
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg		Asp	Ala	Pro	Gln	His	Phe				
				995						1000					1005				
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu		Lys	Tyr	Leu	Phe	Ile	Leu				
				1010						1015					1020				
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu		Ala	Ala	Ser	Ile	Leu	Arg				
				1025						1030					1035				
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe		Ala	Pro	Lys	Phe	Ile	Phe				
				1040						1045					1050				
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser		Val	Gly	Leu	Leu	Leu	Gly				
				1055						1060					1065				
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly		Ala	Val	Ser	Ser	Trp	Phe				
				1070						1075					1080				

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
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gcagttccct gtgtctctgg tggtttgccct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact taaactgtgc agtatttcat cacaaattgg 200  
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350  
taaatacaac agaacgtggc cccagtgtgt gaccaaccac acgctgggtc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450  
gtcccagggc cccctcgccg tgtcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550  
atgttttgcc catatctatt accgtgtttc tttttctgt gatgggctat 600  
tccatctacc gatatatcca cgttgcaaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggaacct gaggccct caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcaccagc aagagtcctt 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050  
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ggcagctctg gggccgcaaa cggtacagta ctatacacc cctcagctcc 1150  
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccg 1200  
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300  
 agccttctga gggggatggg ctcgagagagg agggctcttct atctagactc 1350  
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400  
 catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450  
 gccaacactt ccttttgcct tttgtttcct gtgcaaacia gtgagtcacc 1500  
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550  
 ttgtcagtggt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atggtgggcc 1650  
 tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700  
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys	1	5	10	15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu	20	25	30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr	35	40	45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser	50	55	60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu	65	70	75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His	80	85	90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165	

Ile His Val Gly	Lys Glu Lys His Pro	Ala Asn Leu Ile Leu	Ile
	170	175	180
Tyr Gly Asn Glu Phe	Asp Lys Arg Phe	Phe Val Pro Ala Glu	Lys
	185	190	195
Ile Val Ile Asn Phe	Ile Thr Leu Asn	Ile Ser Asp Asp Ser	Lys
	200	205	210
Ile Ser His Gln Asp	Met Ser Leu Leu	Gly Lys Ser Ser Asp	Val
	215	220	225
Ser Ser Leu Asn Asp	Pro Gln Pro Ser	Gly Asn Leu Arg Pro	Pro
	230	235	240
Gln Glu Glu Glu Glu	Val Lys His Leu	Gly Tyr Ala Ser His	Leu
	245	250	255
Met Glu Ile Phe Cys	Asp Ser Glu Glu	Asn Thr Glu Gly Thr	Ser
	260	265	270
Leu Thr Gln Gln Glu	Ser Leu Ser Arg	Thr Ile Pro Pro Asp	Lys
	275	280	285
Thr Val Ile Glu Tyr	Glu Tyr Asp Val	Arg Thr Thr Asp Ile	Cys
	290	295	300
Ala Gly Pro Glu Glu	Gln Glu Leu Ser	Leu Gln Glu Glu Val	Ser
	305	310	315
Thr Gln Gly Thr Leu	Leu Glu Ser Gln	Ala Ala Leu Ala Val	Leu
	320	325	330
Gly Pro Gln Thr Leu	Gln Tyr Ser Tyr	Thr Pro Gln Leu Gln	Asp
	335	340	345
Leu Asp Pro Leu Ala	Gln Glu His Thr	Asp Ser Glu Glu Gly	Pro
	350	355	360
Glu Glu Glu Pro Ser	Thr Thr Leu Val	Asp Trp Asp Pro Gln	Thr
	365	370	375
Gly Arg Leu Cys Ile	Pro Ser Leu Ser	Ser Phe Asp Gln Asp	Ser
	380	385	390
Glu Gly Cys Glu Pro	Ser Glu Gly Asp	Gly Leu Gly Glu Glu	Gly
	395	400	405
Leu Leu Ser Arg Leu	Tyr Glu Glu Pro	Ala Pro Asp Arg Pro	Pro
	410	415	420
Gly Glu Asn Glu Thr	Tyr Leu Met Gln	Phe Met Glu Glu Trp	Gly
	425	430	435
Leu Tyr Val Gln Met	Glu Asn		
	440		

<210> 105



<211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct  
  
 <400> 105  
     cgctgctgct gttgctcctg g 21  
  
 <210> 106  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 106  
     cagtgtgccca ggactttg 18  
  
 <210> 107  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 107  
     agtcgcaggc agcgttgg 18  
  
 <210> 108  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 108  
     ctcctccgag tctgtgtgct cctgc 25  
  
 <210> 109  
 <211> 51  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaaca 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
cgacgacgtg ggcggacgag tgggcggacg cgtgggtctc tgcggggaga 50  
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tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcggggggc acgaggtgac cccccactcc 200  
agggcctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttctgctg cgagcccgt ggggtgtctc ggccgcccac tgcctcagcc 300  
acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccatga cccacgcaa cgacatctgc ctgtgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcca 500  
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtgctgg 550  
ctggggcttc gtgtctgact ttgaggagct gccgctgga ctgatggagg 600  
ccaaggctcg agtgctggac ccggacgtct gcaacagctc ctggaagggc 650  
cacctgacac ttaccatgct ctgcacccgc agtggggaga gccacagacg 700  
gggcttctgc tcggccgact ccggaggggc cctggtgtgc aggaaccggg 750  
ctcagggcct cgtttccttc tcgggcctct ggtgcggcga cccaagacc 800  
cccgacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850  
ggttcggcgg agcagtcacc agcccgccc cctgcctggg accaccaggc 900  
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
tggtcagggg tggggtggga cgggcagcgg tggggcacac ccattccaca 1050  
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aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
275 280

<210> 112

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 113

cgagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 114

tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

gagctaccca ggcggctggt gtgcagcaag ctccgcgcg actccggacg 50

cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100

cgctgtcggc gctgggcacg gtagcaggcg ccgcccgtgct gctcaaggac 150

tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacagggcat cgggaagcag accgccttgg 250  
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 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400  
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 gtctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
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gagagcaggt gcaggtgtca tcccaggttc aggctctgca cggcatggag 1700  
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<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
 gaagttcgcg agcgcctggca tgtggtcctg gggcgcggtt ggcgcgctg 50  
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
 agcgccggtt gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200  
 cggtgcggg acctgactag attctacgac aaggtacttt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcatTT acttcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400  
 tccagccttt gaggacctg agggagcagc aagggccctg atgcggctgc 450  
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550  
 ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600  
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750  
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
 cccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050  
 tggagcccta cattgctctc taccatgact tcgtcagtga ctgagaggct 1100  
 cagaaaatta gagaacttgc agaaccatgg ctacagaggc cagtgggtggc 1150  
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200  
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250  
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300  
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
 gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450  
 cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500  
 tttggtgga cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550  
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 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700  
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850  
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900  
 ggctgagag ggaagtctct ggagttcaga tactctctgt tgggaacagg 1950  
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000  
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150



tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
1				5					10					15

Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25					30

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40					45

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55					60

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70					75

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85					90

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100					105

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115					120

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130					135

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145					150

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160					165

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175					180

Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly
				185					190					195

Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu
				200					205					210

Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser
				215					220					225

Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala
				230					235					240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser			

Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gacccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagataggga gtctgggttt aagtctctgc tccatctcag gageccctgc 50  
tcccaccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100  
gaatcgggccc tggcagggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
 gctcaagttt tcacttatca tctattccac cgtgttcttg ctgattgggg 300  
 ccttggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400  
 gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
 ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550  
 gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600  
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
 aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
 cgactgcagt gcccctggac ccctggcctg tggggtgccc tacacctgct 750  
 gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
 atcgacaagg agcgtttcag tgtgcaggat gtcattctacg tgcggggctg 850  
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
 gcatcctcct gggcatcctg cttccccagt tcttgggggt gctgctgacg 950  
 ctgtgttaca tcaccgggtt ggaggacatc atcatggagc actctgtcac 1000  
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
 cgggatgctg cttgtgttac cccaattagg gccagcctg ccatggcagc 1100  
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
 ggacagggct gcggcccctc tgcccacact cagtactgac caaagccagg 1200  
 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250  
 agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300  
 gtgcccacct ggggcctggg gaacaaggcc ctcttctc caggcctggg 1350  
 ctacagggga gggagagcct gaggtctgc tcagggccca tttcatctct 1400  
 ggagtgctt tggcgttggg attcaaggca gttttgtagc acctgtaatt 1450  
 ggggagaggg agtgtgcccc tcggggcagg aggggaaggc atctggggaa 1500  
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggttggc 1550  
 ctcttctcag cctcccagggt gccttgagcc ctcttgcaag ggcggtgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асаатааааа 1750  
 catgttttgt tttgttttta аааааааа 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
   1                  5                  10                  15  
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
                   20                  25                  30  
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
                   35                  40                  45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
                   50                  55                  60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
                   65                  70                  75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
                   80                  85                  90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
                   95                  100                  105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
                   110                  115                  120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
                   125                  130                  135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
                   140                  145                  150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
                   155                  160                  165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
                   170                  175                  180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
                   185                  190                  195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
                   200                  205                  210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
                   215                  220                  225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
				245					250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
				260					265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
				275					280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
				290										

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtcc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcatttatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggcgg gcccgaggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150  
tgcaattctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtcctgaagc acatcatctg gctgaaggtc atcacagcta 350  
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggtgga ttcaacacgc ccctggtcaa 450  
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500  
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accagccatg ggagcctgag catccaactg ctgtataagc tctccttctt 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctggtg aagggtgcca tttccctcag 750  
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accaagtggc tcaataactc tgcaagcttc ctgacaatgc ccacctgga 900  
caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950  
tggtgctgtg gctctctcca gaagaattca tggctctgtt ggactctgtg 1000  
cttcctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc 1100  
aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150  
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caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
gatctggggt ccagtgatca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500  
gaaacccagc tctcctgtct cccagtgaag acttggtggtg cagccatcag 1550  
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600  
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	



Ser	Ile	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys	230	235	240
Gly	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp	Ser	245	250	255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser	Leu	260	265	270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val	Ser	275	280	285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro	Glu	290	295	300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala	His	305	310	315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala	Asp	320	325	330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp	Thr	335	340	345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln	Leu	350	355	360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro	Leu	365	370	375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr	Thr	380	385	390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser	Asp	395	400	405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro	Asp	410	415	420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu	Leu	425	430	435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser	Leu	440	445	450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr	Lys	455	460	465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser	Ser	470	475	480
Pro Val Ser Gln																	

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129

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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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				20					25					30
Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35					40					45
Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
				50					55					60
Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
				65					70					75
Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
				80					85					90
Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
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Tyr Ser Ser Ala	Phe Thr Asn Arg Ile	Phe Phe Ala Met Val	Asp
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Phe Asp Glu Gly	Ser Asp Val Phe Gln	Met Leu Asn Met Asn	Ser
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Ala Pro Thr Phe	Ile Asn Phe Pro Ala	Lys Gly Lys Pro Lys	Arg
140	145		150
Gly Asp Thr Tyr	Glu Leu Gln Val Arg	Gly Phe Ser Ala Glu	Gln
155	160		165
Ile Ala Arg Trp	Ile Ala Asp Arg Thr	Asp Val Asn Ile Arg	Val
170	175		180
Ile Arg Pro Pro	Asn Tyr Ala Gly Pro	Leu Met Leu Gly Leu	Leu
185	190		195
Leu Ala Val Ile	Gly Gly Leu Val Tyr	Leu Arg Arg Ser Asn	Met
200	205		210
Glu Phe Leu Phe	Asn Lys Thr Gly Trp	Ala Phe Ala Ala Leu	Cys
215	220		225
Phe Val Leu Ala	Met Thr Ser Gly Gln	Met Trp Asn His Ile	Arg
230	235		240
Gly Pro Pro Tyr	Ala His Lys Asn Pro	His Thr Gly His Val	Asn
245	250		255
Tyr Ile His Gly	Ser Ser Gln Ala Gln	Phe Val Ala Glu Thr	His
260	265		270
Ile Val Leu Leu	Phe Asn Gly Gly Val	Thr Leu Gly Met Val	Leu
275	280		285
Leu Cys Glu Ala	Ala Thr Ser Asp Met	Asp Ile Gly Lys Arg	Lys
290	295		300
Ile Met Cys Val	Ala Gly Ile Gly Leu	Val Val Leu Phe Phe	Ser
305	310		315
Trp Met Leu Ser	Ile Phe Arg Ser Lys	Tyr His Gly Tyr Pro	Tyr
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Ser Phe Leu Met	Ser		
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<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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 <211> 536  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
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 35 40 45  
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
 50 55 60  
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

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 <211> 1475  
 <212> DNA  
 <213> Homo sapiens

<400> 133  
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 ctacatccta ggccttctgg ggcttttggg cacactggtt gccatgctgc 200  
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 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400  
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450



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 actccacagt gtccagacta atttgatgc gaactgaaat aaaaccatcc 1400  
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 gcagcctggg acatttaaaa aaata 1475

<210> 134  
 <211> 230  
 <212> PRT  
 <213> Homo sapiens

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 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
 35 40 45  
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50										55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala					
				65					70					75					
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile					
				80					85					90					
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr					
				95					100					105					
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala					
				110					115					120					
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro					
				125					130					135					
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro					
				140					145					150					
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile					
				170					175					180					
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr					
				185					190					195					
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg					
				200					205					210					
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser					
				215					220					225					
Leu	Thr	Gly	Tyr	Val															
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<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
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<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
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                     20                    25                    30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
                     35                    40                    45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
                     50                    55                    60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
                     65                    70                    75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
                     80                    85                    90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
                     95                    100                    105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
                     110                    115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtgggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
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ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
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 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser	110													

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200  
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<210> 140  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 140  
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 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
 35 40 45  
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
 50 55 60  
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
 65 70 75  
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
 80 85 90  
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
 95 100 105  
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
 110 115 120  
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
 125 130 135  
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

	140		145		150
Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met Glu			
	155		160		165
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val Val			
	170		175		180
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala Ala			
	185		190		195
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro Leu			
	200		205		210
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn Arg			
	215		220		225
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly Ile			
	230		235		240
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile Pro			
	245		250		255
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg Gln			
	260		265		270
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr Pro			
	275		280		285
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu Asp			
	290		295		300
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile			
	305		310		

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ccttctgccc ctcctttcct gccaccgct gcttctcggc 150  
 ccttctccga ccccgtcta gcagcagacc tcctggggtc tgtgggttga 200  
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 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
accgcctcca ctgtccgcct gtccactgcc ccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
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agatcttcag tgcccatgag ctgttcccct ccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgccag caccctccc actgccagac tcctgctgcc 800  
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900  
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actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
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tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200  
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gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
ctcgtccaca catcggatc cccaagccca gacaacctgc gtcgctttgc 1350  
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taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
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cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens  
<400> 142



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				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

	290	295	300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro
	305	310	315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg
	320	325	330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser
	335	340	345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala
	350	355	360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu
	365	370	375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His
	380	385	390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala
	395	400	405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro
	410	415	420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala
	425	430	435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys
	440	445	450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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tgggctacgc gtcctcgtt atcgtgaccc cgggagagcg gcggaagcag 200
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cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400
gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

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 ttttaaggctc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
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<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
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                     20                    25                    30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
                     35                    40                    45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
                     50                    55                    60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
                     65                    70                    75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
                     80                    85                    90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 caggctgcc a tggggcccag caccctctc ctcatcttgt tccttttgtc 150  
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 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
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ttttcccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250  
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
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ttcctcattc ttcaaatgtg ggccagttgt ggctcaaact ctctatattt 1450  
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ccagatcctg agtaatcctt ttagagcccg aagagtcaa accctcaatg 1550  
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acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
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Val

<210> 147

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 147

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gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
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<210> 148  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 148  
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 Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
 35 40 45  
 Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
 50 55 60  
 Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
 65 70 75  
 Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
 80 85 90  
 Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
 95 100 105  
 Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
 110 115 120  
 Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
 125 130 135  
 Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
 140 145 150  
 Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
 155 160 165  
 Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
 170 175 180  
 Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
 185 190 195  
 Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
 200 205 210  
 Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
 215 220 225  
 Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu



230					235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys
				245										255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260										270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275										285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290										300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305										315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320										330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val
				335										345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp
				350										360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His
				365										375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr
				380										390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr
				395										405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe
				410										420
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg
				425										435
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn
				440										450
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu
				455										465
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu
				470										480
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln	Ala	Thr	Thr	Pro	Phe	Leu
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Pro	Arg	Gly	Glu	Met										
				500										

<210> 149

<211> 24

<212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 149  
 gcgtggtcca cctctacagg gacg 24  
  
 <210> 150  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.  
  
 <400> 150  
 ggaactgacc cagtgtgac acc 23  
  
 <210> 151  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 151  
 gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45  
  
 <210> 152  
 <211> 2294  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 152  
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 aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150  
 gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgctcagcc 200  
 gcctcggcgg ggaatgtcac cggcggcggc gggccgcggg ggcaggtgga 250  
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 accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
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<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn			
	185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr			
	200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys			
	215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu			
	230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro			
	245	250	255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tggttggaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
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 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtaggcctc 150  
 ccgggaaaag ggctttgcc aaggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
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 ggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
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 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
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<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
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 gtaaactgct gacgatgcag agttccgtga cggatgcagga aggcctgtgt 150  
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 atgaattatg tgcagagtga aaagcacaca ggctttagag tcaaagtatc 1600  
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 acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

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Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val
				20					25				30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser
				35					40				45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly
				50					55				60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val
				65					70				75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp
				80					85				90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu
				95					100				105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Arg



110										115					120				
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu					
				125					130					135					
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile					
				140					145					150					
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser					
				155					160					165					
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp					
				170					175					180					
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser					
				185					190					195					
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser					
				200					205					210					
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn					
				215					220					225					
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr					
				230					235					240					
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly					
				245					250					255					
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu					
				260					265					270					
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu					
				275					280					285					
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser					
				290					295					300					
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala					
				305					310					315					
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln					
				320					325					330					
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val					
				335					340					345					
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe					
				350					355					360					
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys					
				365					370					375					
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu					
				380					385					390					
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr					
				395					400					405					

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala  
                     410                    415                    420  
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser  
                     425                    430                    435  
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu  
                     440                    445                    450  
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg  
                     455                    460

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagt 200  
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250  
 gaggaggagat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggacct ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcct 650  
 gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
     1                    5                    10                    15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
				35					40						45				
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
				50					55						60				
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
				65					70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
				80					85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
				95					100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
				110					115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
				125					130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
				140					145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
				155					160					165					
Cys	Val	Pro	Glu	His															
				170															

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-21  
 <223> Synthetic construct.  
  
 <400> 165  
 gtcctccgga aagtccttat c 21  
  
 <210> 166  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 166  
 gcctagtgtt cggaacgca gcttc 25  
  
 <210> 167  
 <211> 50  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.  
  
 <400> 167  
 cagggaacctg gtacgtgaag gccatggtgg tcgataagga cttccggag 50  
  
 <210> 168  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 168  
 ctgtccttca ccctggagga ggaggatatc acaggacct ggtac 45  
  
 <210> 169  
 <211> 1204  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 169

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gttccgcaga tgcagagggt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350
ctgtgagcag acccggacag cactgagtc cttccccac ccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
ctcacgtgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag ccccagtta cgctgcctc acacctgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggggta ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggaccaccc caccacagcc catcacctc catttcact 900
tggtgtttgg ttcctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

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<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

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Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
  1               5               10              15

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Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc gggcg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtc 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400



ggcaagattc caccggatgc tacattgatt tttagattg aactttatgc 450  
 tgtgaccaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaaca 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctggt 850  
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
 1 5 10 15  
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
 20 25 30  
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 181  
 gtgttctgct ggagccgatg cc 22

<210> 182  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 182  
 gacatggaca atgacagg 18

<210> 183  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 183  
 cctttcagga tgtaggag 18

<210> 184  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 184  
 gatgtctgcc accccaag 18  
  
 <210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.  
  
 <400> 185  
 gcatcctgat atgacttgct acgtggc 27  
  
 <210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 186  
 tacaagaggg aagaggagtt gcac 24  
  
 <210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.  
  
 <400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
  
 cc 52  
  
 <210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 188  
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 ctctttggag ctgtgactca gaaaacaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150  
 atactttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200  
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250  
 aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
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 1 5 10 15  
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
 20 25 30  
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
 35 40 45  
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
 50 55 60  
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
 65 70

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 190  
 agggaccatt gcttcttcca ggcc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 191  
cgttacatgt ctccaagggg aatg 24

<210> 192  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 192  
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
<211> 1091  
<212> DNA  
<213> Homo sapiens

<400> 193  
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50  
gggtggggggc acagggaaag ggtgacctct gagattcccc tttccccca 100  
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150  
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
gtgtggggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
gcctgcgctg cggggggtgc cttattgacc acaggtgggt cctcacagcg 300  
gctcactgca gcggcagcag gtactgggtg cgcctggggg aacacagcct 350  
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
cccatcccg ctaacctggga gcctcgacga gccacgagca cgacctccgg 450  
ctgtctgggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550  
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
cgggagaatc acgagcaaca tgggtgtgtc aggcggcgtc ccggggcagg 700  
atgcctgcca gggtgattct gggggccccc tgggtgtgtg gggagtcctt 750  
caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttcctcca cctccacccc caccoccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttggaac ttttaactcct 1000  
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050  
 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150  
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350  
 caagaccacac ctggagatga agaagatgat ctgagagtg acaggagggg 400  
 tcagtgcacac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600  
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgtttggg cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700  
 agcacaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750  
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800  
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850  
 cttccagcct gtgttcccct cacttggagg aaccagcact ctccatcctt 900  
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gaccccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000  
 cctctttcgg gtttccttgg acagtgccat ggttcagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
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 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250  
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 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
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 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe	1	5	10	15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn	20	25	30	
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	35	40	45	
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	50	55	60	
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	65	70	75	
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys	80	85	90	
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr	95	100	105	
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu	110	115	120	
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro	125	130	135	
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro	140	145	150	

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens



<400> 197

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ggggtcggcg ccgccgtgcg cgcccgctg gcgctggcct tggcgtggc 150  
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
gctccgctgc cagcgtggac tgccaagggc tgggcctccg cgcggttct 250  
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300  
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350  
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400  
gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450  
ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500  
tgagtgaaaa ccagatccag gggatcccg ggaaggcgtt ccgcggcatc 550  
accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600  
agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650  
acaacaacat cagtcgcac cttggtcacca gcttcaacca catgccgaag 700  
atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750  
ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800  
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cagaagaagg agtacgtgtg ccagcccc cactcggagc ccccatcctg 900  
caatccaac tccatctct gcccttcgcc ctgcacgtgc agcaataaca 950  
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gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050  
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 gcgcatcagc cagatcaaga gcaagaagtt ccgctgctca ggctccgagg 1550  
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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn Asn His Ile	Ser Cys Ile Glu Asp Gly	Ala Phe Arg Ala Leu
170	175	180
Arg Asp Leu Glu Ile	Leu Thr Leu Asn Asn Asn Ile Ser	Arg
185	190	195
Ile Leu Val Thr	Ser Phe Asn His Met Pro Lys Ile Arg Thr	Leu
200	205	210
Arg Leu His Ser	Asn His Leu Tyr Cys Asp Cys His Leu Ala	Trp
215	220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	
230	235	240
Leu Cys Met Ala	Pro Val His Leu Arg Gly Phe Asn Val Ala	Asp
245	250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	
260	265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	
275	280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	
290	295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	
305	310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	
320	325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	
335	340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	
350	355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	
365	370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	
380	385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	
395	400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	
410	415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	
425	430	435
Gln Asn Pro Phe	Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	
440	445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser	

455					460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser
				470					475					480
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe
				485					490					495
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg
				500					505					510
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg
				515					520					525
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn
				530					535					540
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys
				545					550					555
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys
				560					565					570
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu
				575					580					585
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val
				590					595					600
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn
				605					610					615
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser
				620					625					630
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr
				635					640					645
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu
				650					655					660
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly
				665					670					675
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys
				680					685					690
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala
				695					700					705
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln
				710					715					720
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val
				725					730					735
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met
				740					745					750

Pro Lys Asp Val Thr	Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
755		760	765
Ala Val Pro Arg Glu	Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
770		775	780
Asp Leu Ser Asn Asn	Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
785		790	795
Ser Asn Met Ser His	Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
800		805	810
Leu Arg Cys Ile Pro	Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
815		820	825
Arg Val Leu Thr Leu	His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
830		835	840
Gly Ser Phe Asn Asp	Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
845		850	855
Thr Asn Pro Leu His	Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
860		865	870
Trp Val Lys Ala Gly	Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
875		880	885
Ser Pro Glu Pro Met	Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr
890		895	900
His Arg Phe Gln Cys	Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905		910	915
Lys Cys Asn Ala Cys	Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
920		925	930
Cys Thr Gln Asp Pro	Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
935		940	945
Ser Tyr Lys Gly Lys	Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
950		955	960
Gln Asn Pro Cys Gln	His Gly Gly Thr	Cys His Leu Ser Asp	Ser
965		970	975
His Lys Asp Gly Phe	Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
980		985	990
Gln Arg Cys Glu Ile	Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
995		1000	1005
Glu Asn Asn Ala Thr	Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
1010		1015	1020
Ile Cys Pro Pro Asn	Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
1025		1030	1035
Asp His Cys Val Pro	Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly 1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala 1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly 1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu 1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln 1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu 1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu 1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu 1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln 1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335



Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
 1340 1345 1350  
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
 1355 1360 1365  
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
 1370 1375 1380  
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
 1385 1390 1395  
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
 1400 1405 1410  
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
 1415 1420 1425  
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
 1430 1435 1440  
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
 1445 1450 1455  
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
 1460 1465 1470  
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
 1475 1480 1485  
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
 1490 1495 1500  
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
 1505 1510 1515  
 Glu Cys Gly Cys Leu Ala Cys Ser  
 1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttagttct gtctccgga ggctttgagg atgaaggctg 150  
cgggcattct gacctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccggt ttctcccaa tattccttct caaacttga 700  
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750  
gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
     1                    5                    10                    15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
                     20                    25                    30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
                     35                    40                    45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
                     50                    55                    60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
                     65                    70                    75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
                     80                    85                    90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
                     95                    100                    105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
                     110                    115                    120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
                     125                    130                    135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
                     140                    145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
 ctcatagggt gcctgggtcac aggc 24

<210> 206  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 206  
 ccagtcggac aggtctctcc cctc 24

<210> 207  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 207  
 tcagtaccca aggtgagca ggcg 24

<210> 208  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 208  
 ctacactcgt tgcaaacctgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209  
 <211> 1648  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 caggccattt gcatcccact gtccttgtgt tcggagccag gccacaccgt 50  
 cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
 tattaataact tgtacatggc tcccattgg tttttggaga aaagttcaag 150  
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
 gcggaagaag atcctatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
 gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctgagttggt 450  
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550  
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600  
 catctgatcg tggcagggtg ttatgacgag agagtccctg agaattgtgga 650  
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
 atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctctc 750  
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
 tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900  
 gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950  
 accttcctta aaagccacca tgggcctggc tgggaagagc agagtgaagg 1000  
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050  
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100  
 ttatggattg tagaccagtt tttgaaacca aaaaagaaac ctagaatcta 1150  
 atgcagaaga gatcttttaa aaaataaaact tgagtcttga atgtgagcca 1200  
 ctttcttata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300  
 tgtcattcca tgttcagcag agtattttaa ttatattttc tcgggattat 1350  
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gttcatagt 1450  
 ataattgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500  
 tcaactgtcat ctgttaggga atttttgttt gtccgtgtct tgccctggatc 1550  
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
1				5					10					15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
				20					25					30
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35					40					45
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50					55					60
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65					70					75
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80					85					90
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95					100					105
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110					115					120
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125					130					135
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140					145					150
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
				155					160					165
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg
				170					175					180
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val
				185					190					195
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe
				200					205					210
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val
				215					220					225
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu
				230					235					240
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly
				245					250					255
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu
				260					265					270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens

<400> 211  
gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
cttcgcgatc ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
tttgcattgag ttcctgggta atttgcattg gagatatggg cctgtggtct 250  
ccttctggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300  
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350  
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
gttttgctat gaagtctgtt acacagattg taatgggtag tacatttgaa 600  
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650  
tgagattgga aaaggcttct tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
tgactcctta gtacaaggga acctaatga ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgaggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050  
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100  
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150  
 tgg tacttca ggatcctaact acttggccat ctccacacaa gtttgatcca 1200  
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggtt 1250  
 ctccaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300  
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350  
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400  
 agcttggtatc actgtctcaa agagatatta aaattttata catttaaaat 1450  
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500  
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550  
 ttaa 1554

<210> 212  
 <211> 462  
 <212> PRT  
 <213> Homo sapiens

<400> 212  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu  
 1 5 10 15  
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala  
 20 25 30  
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu  
 35 40 45  
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn  
 50 55 60  
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg  
 65 70 75  
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His  
 80 85 90  
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys  
 95 100 105  
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn  
 110 115 120  
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu  
 125 130 135  
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu



	140		145		150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	155	Gln His Val Pro Leu Ser	160		165
Gln His Met Leu Gly Phe Ala Met Lys	170	Ser Val Thr Gln Met Val	175		180
Met Gly Ser Thr Phe Glu Asp Asp Gln	185	Glu Val Ile Arg Phe Gln	190		195
Lys Asn His Gly Thr Val Trp Ser Glu	200	Ile Gly Lys Gly Phe Leu	205		210
Asp Gly Ser Leu Asp Lys Asn Met Thr	215	Arg Lys Lys Gln Tyr Glu	220		225
Asp Ala Leu Met Gln Leu Glu Ser Val	230	Leu Arg Asn Ile Ile Lys	235		240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	245	His Ile Phe Ile Asp Ser	250		255
Leu Val Gln Gly Asn Leu Asn Asp Gln	260	Gln Ile Leu Glu Asp Ser	265		270
Met Ile Phe Ser Leu Ala Ser Cys Ile	275	Ile Thr Ala Lys Leu Cys	280		285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	290	Ser Glu Glu Val Gln Lys	295		300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	305	Phe Gly Asn Gly Pro Val	310		315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	320	Tyr Cys Gln His Val Leu	325		330
Cys Glu Thr Val Arg Thr Ala Lys Leu	335	Thr Pro Val Ser Ala Gln	340		345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	350	Arg Phe Ile Ile Pro Arg	355		360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	365	Val Val Leu Gln Asp Pro	370		375
Asn Thr Trp Pro Ser Pro His Lys Phe	380	Asp Pro Asp Arg Phe Asp	385		390
Asp Glu Leu Val Met Lys Thr Phe Ser	395	Ser Leu Gly Phe Ser Gly	400		405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	410	Ala Tyr Met Val Thr Thr	415		420
Val Leu Leu Ser Val Leu Val Lys Arg	425	Leu His Leu Leu Ser Val	430		435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
455 460

<210> 213  
<211> 759  
<212> DNA  
<213> Homo sapiens

<400> 213  
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tccagcctca gagaccgccg cccttgtccc cgagggccat gggccgggtc 100  
tcagggttg tgccctctcg ctctctgacg ctcttgccgc atctggtggt 150  
cgtcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200  
ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300  
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
gggtcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400  
tgggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450  
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
ttccctcgg aaactgcttc tgctggagga tatgtgttg aataattacg 650  
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750  
aaaaaaaa 759

<210> 214  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 214  
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
1 5 10 15  
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
20 25 30  
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccggaccc tgccgccctg ccactatgtc ccgccgtct atgctgcttg 50  
 cctgggctct cccagcctc ctctgactcg gagcggtca ggagacagaa 100  
 gaccggcct gctgcagccc catagtgcc cggaacgagt ggaaggcct 150  
 ggcacagag tgcgccagc acctgagcct gcccttacgc tatgtggtg 200  
 tatcgacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctgggtcga 300  
 cgtgggtac aacttcctga ttggagaaga cgggctcgt tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcac gggcaactac atggatcggg tgccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggctgcggt gtggctcagg 500  
 gagccctgag gtccaactat gtgctcaaag gacaccgga tgtgcagcgt 550  
 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

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 1           5          10          15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
          20          25          30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
          35          40          45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
          50          55          60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
          65          70          75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
          80          85          90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
          95         100         105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
          110         115         120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
          125         130         135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
          140         145         150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
          155         160         165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
          170         175         180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
          185         190         195
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Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
tctatctggt catctgtggc caggatgatg gtcctcccgg ctgagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgctcggaa 200
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gcggggccac atctcaccta agtcccgcct catggccaat tccactctcc 250  
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350  
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400  
 tgctcgtcac aggaagatt gtggacctat gcaatgggac cttcagcgtc 450  
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500  
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<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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				20					25					30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	
				35					40					45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	
				50					55					60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	
				65					70					75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	
				80					85					90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	
				95					100					105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	
				110					115					120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	
				125					130					135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	
				140					145					150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	
				155					160					165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	
				170					175					180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	
				185					190					195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	
				200					205					210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
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Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
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Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20					25					30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35					40					45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50					55					60



Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
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				200											

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 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-20  
 <223> Synthetic construct.

<400> 221  
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<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 222  
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<210> 223  
 <211> 40

<212> DNA  
 <213> Artificial  
 <220>  
 <221> Artificial Sequence  
 <222> 1-40  
 <223> Synthetic construct.

<400> 223  
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<210> 224  
 <211> 902  
 <212> DNA  
 <213> Homo sapiens

<400> 224  
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 tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150  
 tttcgtccct tgtttggttc atggcaagag tcattattga caacaagat 200  
 ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
 tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
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 tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
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<210> 225  
 <211> 257  
 <212> PRT

<213> Homo sapiens

<400> 225

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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	
				20					25					30	
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50					55					60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95					100					105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
				110					115					120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125					130					135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140					145					150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155					160					165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170					175					180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185					190					195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200					205					210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215					220					225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230					235					240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226  
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln  
                           20                          25                          30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615



Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn	620	625	630
Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr	635	640	645
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu	650	655	660
Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp	665	670	675
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val	680	685	690
Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr	695	700	705
Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala	710	715	720
Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile	725	730	735
Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu	740	745	750
Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe	755	760	765
Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser	770	775	780
Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp	785	790	795
His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser	800	805	810
Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln	815	820	825
Arg Asp Lys Ile Tyr Val Phe	830		

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttgggcgctg gagggcctgt cctgaccatg gtcctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggtctctcc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaattttccc tttataacctg 250  
 accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc 300  
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20					25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro
				35					40					45
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
				80					85					90
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
				95					100					105
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
				110					115					120
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
				125					130					135
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
				140					145					150
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
				155					160					165
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
				170					175					180
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
				185					190					195
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
				200					205					210
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
				215					220					225
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
				230					235					240
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
				245					250					255
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
				260					265					270
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
				275					280					285
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
				290					295					300
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
				305					310					315

Tyr Ala Ala Pro	Leu Glu Leu His Val	Leu Val Met Asp Glu Asn	320	325	330
Asp Asn Val Pro	Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile	335	340	345
Pro Glu Leu Ser	Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala	350	355	360
Glu Asp Ala Asp	Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr	365	370	375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg Ala	380	385	390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val Leu	395	400	405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala Met	410	415	420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu Val	425	430	435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe Ile	440	445	450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu Pro	455	460	465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu Glu	470	475	480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp Thr	485	490	495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His Val	500	505	510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro Ser	515	520	525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val Gly	530	535	540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu Val	545	550	555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr Glu	560	565	570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu Thr	575	580	585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser Leu	590	595	600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser Gly			

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
800	805	

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 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-50  
 <223> Synthetic construct.

<400> 230  
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<210> 231  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> Artificial Sequence  
 <222> full  
 <223> Synthetic oligonucleotide probe

<400> 231  
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<210> 232  
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 <213> Artificial Sequence

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<400> 232  
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<210> 233  
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 <212> DNA  
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 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
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 tagacaatga agatgatgaa atgcaacaca atgaaggga agaacggagc 350  
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 agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500  
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 <211> 421  
 <212> PRT  
 <213> Homo sapiens

<400> 234  
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 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn  
 35 40 45  
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe  
 50 55 60  
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala  
 65 70 75  
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr  
 80 85 90  
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met  
 95 100 105  
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr  
 110 115 120  
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn  
 125 130 135  
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly  
 140 145 150  
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr  
 155 160 165

Gly Lys Gly Val	Arg Arg Pro Ala Val	Trp Leu Asn Ala Gly Ile	170	175	180
His Ser Arg Glu	Trp Ile Ser Gln Ala	Thr Ala Ile Trp Thr Ala	185	190	195
Arg Lys Ile Val	Ser Asp Tyr Gln Arg	Asp Pro Ala Ile Thr Ser	200	205	210
Ile Leu Glu Lys	Met Asp Ile Phe Leu	Leu Pro Val Ala Asn Pro	215	220	225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln	Asn Arg Leu Trp Arg Lys	230	235	240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser	Cys Ile Gly Ala Asp Pro	245	250	255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala	Gly Lys Gly Ala Ser Asp	260	265	270
Asn Pro Cys Ser	Glu Val Tyr His Gly	Pro His Ala Asn Ser Glu	275	280	285
Val Glu Val Lys	Ser Val Val Asp Phe	Ile Gln Lys His Gly Asn	290	295	300
Phe Lys Gly Phe	Ile Asp Leu His Ser	Tyr Ser Gln Leu Leu Met	305	310	315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys	Ala Pro Asp Ala Glu Glu	320	325	330
Leu Asp Lys Val	Ala Arg Leu Ala Ala	Lys Ala Leu Ala Ser Val	335	340	345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro	Thr Cys Thr Thr Val Tyr	350	355	360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp	Ala Tyr Asp Asn Gly Ile	365	370	375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg	Asp Thr Gly Thr Tyr Gly	380	385	390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile	Pro Thr Ala Glu Glu Thr	395	400	405
Trp Leu Gly Leu	Lys Thr Ile Met Glu	His Val Arg Asp Asn Leu	410	415	420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100  
ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200  
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
gagtcagaac atcttcttct ccctgtgag tgtctccact tccctggcca 300  
tgctctccct tggggccac tcagtcacca agaccagat tctccagggc 350  
ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
ccagcacctg gttcactcac tgactgttcc cagcaaagac ctgaccttga 450  
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tttctccaac cctctcattg cccaggcgag gatcaacagc catgtgaaaa 600  
agaagacca aggaagggtt gtagacataa tccaaggcct tgaccttctg 650  
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gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
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cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
tgcacaagaa ataacaaacc acatccctct ttctgttctg agggatgcatt 1400  
tgacccaggt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450

aatcaccaaa ccatcaacag ggacccagc cacaagccaa caccattaa 1500  
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 ggatgttgct gggttaccat atttcattc cttggggctc ccaggaatgg 1600  
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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
     1                    5                    10                    15  
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
                     20                    25                    30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
                     35                    40                    45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
                     50                    55                    60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
                     65                    70                    75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
                     80                    85                    90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
                     95                    100                    105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
                     110                    115                    120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
                     125                    130                    135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
                     140                    145                    150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
                     155                    160                    165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
                     170                    175                    180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
                     185                    190                    195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn	Phe		
	215	220	225		
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met	Met		
	230	235	240		
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn			
	245	250	255		
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala	Phe		
	260	265	270		
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln	Ala		
	275	280	285		
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln	Lys		
	290	295	300		
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala	Ser		
	305	310	315		
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn	Ala		
	320	325	330		
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp	Ser		
	335	340	345		
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val	Ser		
	350	355	360		
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe	Ile		
	365	370	375		
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe	Asn		
	380	385	390		
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly	Ile		
	395	400	405		
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410	415			

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.  
  
 <400> 238  
 ctttgctggtt ggcctctgtg ctccaacca tgcaaggaca gggcagg 47  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 239  
 tgactcgggg tctccaaaac cagc 24  
  
 <210> 240  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 240  
 ggtataggcg gaaggcaaag tcgg 24  
  
 <210> 241  
 <211> 48  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.  
  
 <400> 241  
 ggcacatctac ctttatggag tactctttgc tgttggcctc tgtgctcc 48  
  
 <210> 242  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 242  
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 gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150  
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200  
 ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
 aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300  
 aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350  
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
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 cacactctcc agtggggcca gcacagccac caactctgac tccagcacia 800  
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<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25				30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40				45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55				60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70				75	



Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365	370	375
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
	380	385	390
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala
	395	400	405
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
	410	415	420
Thr Asn Ser Asp	Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala
	425	430	435
Thr Asn Ser Glu	Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val
	440	445	450
Thr Asn Ser Glu	Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala
	455	460	465
Thr Asn Ser Gly	Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala
	470	475	480
Ala Leu Thr Gly	Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala
	485	490	495
Val Ser Glu Ala	Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile
	500	505	510
Phe Leu Ile Thr	Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe
	515	520	525
Ala Gly Leu Phe	Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn
	530	535	540
Thr Phe Asn Thr	Ala Val Tyr His Pro	His Gly Leu Asn His	Gly
	545	550	555
Leu Gly Pro Gly	Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro
	560	565	570
Arg Trp Ser Pro	Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile
	575	580	585
Ala Met Glu Met	Ser Gly Arg Asn Ser	Gly Pro	
	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic sequence.

<400> 245  
gtcagagttg gtggctgtgc tagc 24

<210> 246  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-48  
<223> Synthetic construct.

<400> 246  
ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247  
<211> 957  
<212> DNA  
<213> Homo sapiens

<400> 247  
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ttcccgacct tccagcaat atgcatcttg cacgtctggc cggctcctgc 100  
tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150  
ccccattgag aaggtcattg aagggatcaa ccgaggggtg agcaatgcag 200  
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250  
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300  
ccacaccggc aaggagttag acaaaggcgt ccaggggctc aaccacggca 350  
tggacaaggt tgcccatgag atcaacatg gtattggaca agcaggaaaag 400  
gaagcagaga agcttggcc tgggttcaac aacgctgctg gacaggccgg 450  
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500  
ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550  
caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750  
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
 gttgtcacat cagctgacat gacctggagg gggtgggggt gggggacagg 900  
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 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
 185 190 195  
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
 200 205 210  
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
 215 220 225  
 Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
 230 235 240  
 Ser Val Ala Asn Ile Met Pro  
 245

<210> 249  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 249  
 caatatgcat cttgcacgtc tgg 23

<210> 250  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 250  
 aagcttctct gcttcctttc ctgc 24

<210> 251  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 251  
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<210> 252  
 <211> 3781  
 <212> DNA  
 <213> Homo sapiens

<400> 252

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<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	35	40	45	
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu	50	55	60	
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu	65	70	75	
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu				



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Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
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Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
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Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
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Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
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Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
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Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
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Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
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Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
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Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
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Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
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Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
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Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
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Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
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Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
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Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
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Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu	Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Pro	380	385	390
Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg	395	400	405
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Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser	425	430	435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala	440	445	450
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe	455	460	465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly	470	475	480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly	485	490	495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu	500	505	510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn	515	520	525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp	530	535	540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu	545	550	555
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Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser	605	610	615
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Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu	650	655	660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val			

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Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695		700		705
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
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Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725		730		735
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
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Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
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Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
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 <222> 3635  
 <223> unknown base

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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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				20					25					30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	
				35					40					45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	
				50					55					60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	
				65					70					75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	
				80					85					90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	
				95					100					105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	
				110					115					120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	
				125					130					135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	
				140					145					150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	
				155					160					165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	
				170					175					180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	
				185					190					195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	
				200					205					210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	
				215					220					225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	
				230					235					240	



Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val	Phe
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn
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<211> 24

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 <222> 1-24  
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 <212> DNA  
 <213> Homo sapiens  
  
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
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Leu Leu Lys Val Tyr  
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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				35					40					45					
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
				140					145					150					
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
				155					160					165					
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
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Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					



Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
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 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900  
 aatgcagta catagagttt gtctccctga tgcacccat gagtttcaac 950  
 caggatgatgt gatgtttgtg acaggatttg gagcactgaa aatgatggt 1000  
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 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
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 ggaggaccac tggttagttc agatgctaga gatatctggt accttgctgg 1200  
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 taagagacaa aagcctcatg gaacagataa catttttttt tgtttttttg 1350  
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
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 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
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 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750  
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 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900  
 tccagaaaga agccaagata tctccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050  
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<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
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                     20                    25                    30  
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
                     35                    40                    45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
                     50                    55                    60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
                     65                    70                    75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
                     80                    85                    90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
                     95                    100                    105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
                     110                    115                    120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
                     125                    130                    135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
                     140                    145                    150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
                     155                    160                    165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
                     170                    175                    180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
                     185                    190                    195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
                     200                    205                    210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
                     215                    220                    225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	
				230					235					240	
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	
				245					250					255	
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	
				260					265					270	
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	
				275					280					285	
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	
				290					295					300	
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	
				305					310					315	
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	
				320					325					330	
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	
				335					340					345	
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	
				350					355					360	
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	
				365					370					375	
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	
				380					385					390	
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	
				395					400					405	
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	
				410					415					420	

Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

<400> 270  
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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150  
 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200  
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300  
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350  
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400  
gacccgccgc gcatgggaga agtgcgcatg gcggccgaag agggccgcgc 450  
agtgggtccac tgggtgtgcc ccttctcccc ggtcctccac tactggctgc 500  
tgctttggga cggcagcgag gctgcgcaga aggggcccc gctgaacgct 550  
acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600  
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650  
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agccgccttg cggtgccgcc caacccccgc actctggtcc acgcggccgt 750  
cgggggtggc acggccctgg cctgtctaag ctgtgccgcc ctggtgtggc 800  
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gccgcagggg cgctctgaaa ggggcctggg ggcattctcg gcacagacag 900  
ccccacctgg ggcgctcagc ctggcccccg ggaaagagga aaacccgctg 950  
cctccaggga gggctggacg gcgagctggg agccagcccc aggtccagg 1000  
gccacggcgg agtcatggtt ctcaggactg agcgcttgtt taggtccggt 1050  
acttggcgct ttgtttctg gctgaggtct gggaaggaat agaaaggggc 1100  
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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
			50					55						60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
			65					70						75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu  
 80 85 90  
 Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys  
 95 100 105  
 Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp  
 110 115 120  
 Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val  
 125 130 135  
 Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val  
 140 145 150  
 Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro  
 155 160 165  
 Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe  
 170 175 180  
 Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu  
 185 190 195  
 Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser  
 200 205 210  
 Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly  
 215 220 225  
 Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu  
 230 235

<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
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 cccaggcggg cgtggggcac cgggccagc gccgacgac gctgccgttt 150  
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250  
 acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300  
 tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350  
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 cggtcattgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450  
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aagtttgctt gtcattttct gtgtagaact ggcttggtgc gtttgacat 550  
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cagtgcactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850  
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900  
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950  
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caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200  
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300  
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat 1350  
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aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450  
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atataaagta ctaattaaat gctaacatag gaagttagaa aataactaata 1550  
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cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650  
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taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agastgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000  
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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200  
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 cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300  
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
			20						25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
			35						40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
			50						55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
			65						70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
			80						85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
			95						100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
			110						115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
			125						130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
			140						145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
			155						160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser



170										175					180				
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln					
				185					190					195					
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met					
				200					205					210					
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe					
				215					220					225					
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu					
				230					235					240					
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro					
				245					250					255					
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His					
				260					265					270					
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg					
				275					280					285					
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe					
				290					295					300					
Glu	Met	Glu	Glu	Leu															
				305															

<210> 274  
 <211> 2063  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
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 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgctgc 150  
 cttggggtga caatctcagc tccaggctac agggagaccg ggaggatcac 200  
 agagccagca tgttacagga tctgacagt gatcaacctc tgaacagcct 250  
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 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350  
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 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550  
 ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600

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 aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag 750  
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 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850  
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 tcttcacca tcccaagcc tactagagca agaaaccagt tgtaataata 1950  
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgctatt 2000  
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
260	265	270	
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
275	280	285	
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
290	295	300	
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
305	310	315	
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
320	325	330	
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
335	340	345	
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
350	355	360	
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
365	370	375	
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
380	385	390	
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
395	400	405	
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
410	415	420	
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<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

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Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

290					295					300				
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro
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Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val
				320					325					330
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp
				335					340					345
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu
				350					355					360
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg
				365					370					375
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr
				380					385					390
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr
				395					400					405
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val
				410					415					420
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr
				425					430					435
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly
				440					445					450
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp
				455					460					465
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala
				470					475					480
Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala
				485					490					495
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg
				500					505					510
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu
				515					520					525
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg
				530					535					540
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser
				545					550					555
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala
				560					565					570
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala
				575					580					585



Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu	590	595	600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln	605	610	615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly	620	625	630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln	635	640	645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His	650	655	660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala	665	670	675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu	680	685	690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser	695	700	705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu	710	715	720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His	725	730	735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp	740	745	750
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<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

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<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279  
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<210> 280  
 <211> 45  
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<220>  
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 <222> 1-45  
 <223> Synthetic construct.

<400> 280  
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<210> 281  
 <211> 2320  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
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<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr	20	25	30	
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile	35	40	45	
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg	50	55	60	
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln	65	70	75	
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys	80	85	90	
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly	95	100	105	
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln	110	115	120	
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys	125	130	135	
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys	140	145	150	
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile	155	160	165	
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro	170	175	180	
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met	185	190	195	
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe	200	205	210	
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile	215	220	225	
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu	230	235	240	
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe	245	250	255	
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly				

	260	265	270
Leu Met Glu Lys	Pro Ile Lys Pro Val 275	Pro Gln Asp Leu Glu 280	Asn 285
Phe Ile Ala Lys	Phe Gly Asp Ser Gly 290	Phe Val Leu Val Thr 295	Leu 300
Gly Ser Met Val	Asn Thr Cys Gln Asn 305	Pro Glu Ile Phe Lys 310	Glu 315
Met Asn Asn Ala	Phe Ala His Leu Pro 320	Gln Gly Val Ile Trp 325	Lys 330
Cys Gln Cys Ser	His Trp Pro Lys Asp 335	Val His Leu Ala Ala 340	Asn 345
Val Lys Ile Val	Asp Trp Leu Pro Gln 350	Ser Asp Leu Leu Ala 355	His 360
Pro Ser Ile Arg	Leu Phe Val Thr His 365	Gly Gly Gln Asn Ser 370	Ile 375
Met Glu Ala Ile	Gln His Gly Val Pro 380	Met Val Gly Ile Pro 385	Leu 390
Phe Gly Asp Gln	Pro Glu Asn Met Val 395	Arg Val Glu Ala Lys 400	Lys 405
Phe Gly Val Ser	Ile Gln Leu Lys Lys 410	Leu Lys Ala Glu Thr 415	Leu 420
Ala Leu Lys Met	Lys Gln Ile Met Glu 425	Asp Lys Arg Tyr Lys 430	Ser 435
Ala Ala Val Ala	Ala Ser Val Ile Leu 440	Arg Ser His Pro Leu 445	Ser 450
Pro Thr Gln Arg	Leu Val Gly Trp Ile 455	Asp His Val Leu Gln 460	Thr 465
Gly Gly Ala Thr	His Leu Lys Pro Tyr 470	Val Phe Gln Gln Pro 475	Trp 480
His Glu Gln Tyr	Leu Phe Asp Val Phe 485	Val Phe Leu Leu Gly 490	Leu 495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly 500	Lys Leu Leu Gly Met 505	Ala 510
Val Trp Trp Leu	Arg Gly Ala Arg Lys 515	Val Lys Glu Thr 520	

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 283  
tgcttttgct cacctacccc aagg 24

<210> 284  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 284  
tcaggctggt ctccaaagag aggg 24

<210> 285  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 285  
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<210> 286  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 286  
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cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
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gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400  
ccagggagag gagcggaaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaagccac actggctacc 500  
 aggtccccta cacagtcccg ggctgccctt ggttctggtg cttctggccc 550  
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser	1	5	10	15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly	20	25	30	
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys	35	40	45	
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly	50	55	60	
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala	65	70	75	
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	80	85	90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	95	100	105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	110	115	120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	125	130	135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	140	145	150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	155	160	165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser				



	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
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 tagccgccca gcctcgacgc cgtcccgga cccctgtgct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200  
 ccgctactc cggggtcctg cgcggcgagc gtcaggccga ggctgaccgg 250  
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300  
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 tcacctggct caataggtcc aaggtggaaa agcagctaca ggtcatctca 400  
 gtgctccagt gggctcctgtc cttccttgta ctgggagtgg cctgcagtgc 450  
 catcctcatg tacatattct gcactgattg ctggctcatc gctgtgctct 500  
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 aggtcacagt ggggtccgaaa ctgggctgtg tggcgctact ttcgagacta 600  
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 tttgctctgt aaatttgga gtgtcatggg tgtctgtggg ttatttataa 1450  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550  
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<210> 292  
 <211> 388  
 <212> PRT.  
 <213> Homo sapiens

<400> 292

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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

	260	265	270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val	Tyr
	275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val	Gln
	290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe	His
	305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro	Tyr
	320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly	Glu Pro Ile Thr Ile	Pro
	335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His	Thr
	350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu	Phe Asp Lys His Lys	Thr
	365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val	Leu Glu Val Asn	
	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcggg atggggggccg gggcgggcgg gcgcgcgact cgctgaggcc 50  
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cggggcccg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggcg 150  
gcggtctgag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
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caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtgggtctg 350  
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gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800  
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 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000  
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 agctcaagtg atctgcctgc ttcagcctcc caaagtgctg ggattacaga 2850  
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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacta 2950  
 ccaggagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgag 3050  
 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt ggggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA



<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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 tctgtactaa aaatacaca attagctggg catggtggca catgcctgta 1200  
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<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
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 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200  
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<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

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Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu	20	25	30	
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly	35	40	45	
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly	50	55	60	
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro	65	70	75	
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala	80	85	90	
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly	95	100	105	
Arg Arg Arg Asp																		

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

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 ccgccttcgc cactggcctc ttcctgggga ggcggtgccc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
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 ataaagtggg gctgggacac aaaaaaaaa aaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
			20						25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
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<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met	1	5	10	15
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Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe	35	40	45	
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro	50	55	60	
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys	65	70	75	
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala	80	85	90	
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala	95	100	105	
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp	110	115	120	
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala	125	130	135	
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser				



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Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
	155	160	165
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala
	170	175	180
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu
	185	190	195
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala
	200	205	210
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys
	215	220	225
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser
	230	235	240
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser
	245	250	255
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val
	260	265	270
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro
	275	280	285
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser
	290	295	300
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu
	305	310	315
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg
	320	325	330
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln
	335	340	345
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly
	350	355	360
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg
	365	370	375
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly
	380	385	390
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu
	395	400	405
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser
	410	415	420
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg
	425	430	435

Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
				440					445					450	
Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
				500					505					510	
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
				545					550					555	
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
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Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
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 <212> DNA  
 <213> Homo sapiens

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg	1	5	10	15
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Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	35	40	45		
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	50	55	60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	65	70	75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	80	85	90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	95	100	105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	110	115	120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	125	130	135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu				



140					145					150				
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
				155					160					165
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
				170					175					180
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
				185					190					195
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
				200					205					210
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
				215					220					225
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
				230					235					240
Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
				245					250					255
Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val
				260					265					270
Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala
				275					280					285
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn
				290					295					300
Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu
				305					310					315
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu
				320					325					330
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys
				335					340					345
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala
				350					355					360
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys
				365					370					375
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val
				380					385					390
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser
				395					400					405
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr
				410					415					420
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro
				425					430					435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

	725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp	740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr	755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro	770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg	785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro	800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu	815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys	830	835	

<210> 318  
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 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
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<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cggatgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

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<400> 320
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<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

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<210> 322

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<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

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 275 280 285  
 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
 290 295 300  
 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
 305 310 315  
 Arg Val

<210> 323  
 <211> 1174  
 <212> DNA  
 <213> Homo sapiens

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 ggccgtgcag cttctgggct tcctgctcag cttcctgggc atggtgggca 150  
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 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950  
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
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 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 324  
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 20 25 30  
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser  
 35 40 45  
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly  
 50 55 60  
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu  
 80 85 90  
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu  
 110 115 120  
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala  
 125 130 135  
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro  
 140 145 150  
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr  
 155 160 165  
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu  
 170 175 180  
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln  
 185 190 195  
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala  
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 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val  
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

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Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
				95					100					105
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
				110					115					120
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
				125					130					135
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
				140					145					150
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
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Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
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Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185					190					195
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200					205					210
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215					220					225
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230					235					240
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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<210> 328

<211> 225

<212> FRT

<213> Homo sapiens

<400> 328

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Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
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<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp	
				20					25					30	
Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val	
				35					40					45	
Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	
				50					55					60	
Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val	
				80					85					90	
Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr	
				95					100					105	
Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr	
				110					115					120	
Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro	
				125					130					135	
Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro	
				140					145					150	
Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr	
				155					160					165	
Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu	
				170					175					180	
Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His	
				185					190					195	
Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly	
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Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val						
				215					220						

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

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Ala Leu Met Cys	Val Ala Val Ala Leu Ser	Leu Ile Ala Leu Leu	
	35	40	45
Ile Gly Ile Cys	Gly Met Lys Gln Val Gln	Cys Thr Gly Ser Asn	
	50	55	60
Glu Arg Ala Lys	Ala Tyr Leu Leu Gly Thr	Ser Gly Val Leu Phe	
	65	70	75
Ile Leu Thr Gly	Ile Phe Val Leu Ile Pro	Val Ser Trp Thr Ala	
	80	85	90
Asn Ile Ile Ile	Arg Asp Phe Tyr Asn Pro	Ala Ile His Ile Gly	
	95	100	105
Gln Lys Arg Glu	Leu Gly Ala Ala Leu Phe	Leu Gly Trp Ala Ser	
	110	115	120
Ala Ala Val Leu	Phe Ile Gly Gly Gly Leu	Leu Cys Gly Phe Cys	
	125	130	135
Cys Cys Asn Arg	Lys Lys Gln Gly Tyr Arg	Tyr Pro Val Pro Gly	
	140	145	150
Tyr Arg Val Pro	His Thr Asp Lys Arg Arg	Asn Thr Thr Met Leu	
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Ser Lys Thr Ser	Thr Ser Tyr Val		
	170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys  
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<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

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<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
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35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
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<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150  
ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgaggcgagg 200  
gacccactgc ccagccgctc agggacccca acgccatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300  
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 ggggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400  
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450  
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500  
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 tgtccacgag agtcggtccc ccaaattccc cctgcccgcc ggggtccgag 650  
 cccggcccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700  
 cctgctggtg ctgctgctct ggtactgcca gatccagtac cggcccttct 750  
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 ctctggcct ttgccatgta ccgcccgtag tgcctccgcg ggcgcttggc 850  
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 ctgcctgccc aggccgcct ctccggcctg cctcttcccg ctgccctgga 950  
 gccagccct gcgcgcaga ggactcccgg gactggcgga ggccccgcc 1000  
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050  
 cgcactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100  
 gccccgggca gagccggggc gccccggggg cccgtcttag tgttctgcg 1150  
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 acgccaggtc ggtgggaggc tgggaaggg gagcggggag gggcagagga 1250  
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300  
 aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe  
           1                  5                  10                  15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
                   20                  25                  30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
                   35                  40                  45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	
				50					55					60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	
				65					70					75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	
				80					85					90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	
				95					100					105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	
				110					115					120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	
				125					130					135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	
				140					145					150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	
				155					160					165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	
				170					175					180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	
				185					190					195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	
				200					205					210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	
				215					220					225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	
				230					235					240	
Phe	Ala	Met	Tyr	Arg	Pro										
				245											

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcacagtc gctgtgactt ggcccagggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300  
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 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400  
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450  
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 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700  
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 341  
ccctccaagg atgacaaagg cgc 23

<210> 342  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-29  
<223> Synthetic construct.

<400> 342  
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 343  
atctcaggcg gcatcctgtc agcc 24

<210> 344  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 344  
gtggatgcct gcaagaaggt tggg 24

<210> 345  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtagac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100  
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150  
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200  
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250  
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300  
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aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400  
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545	550	555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val
	560	565	570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln
	575	580	585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser
	590	595	600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu
	605	610	615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe
	620	625	630
Asp Gln Ile Asn	Ala Val Asp Glu Arg		
	635		

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagagggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgtg cgagggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
<211> 2524  
<212> DNA  
<213> Homo sapiens

<400> 351  
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

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 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
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 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
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 230 235 240  
 Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

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 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
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<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
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                     20                    25                    30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
                     35                    40                    45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
                     50                    55                    60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
                     65                    70                    75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
                     80                    85                    90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
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 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
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 Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	125	130	135	
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Ser Pro Arg Gly Asp Leu Pro  
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550
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aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950
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ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
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cagaagttaa aggtgtctc caagtccctg aactcagcag aaatagacca 1450  
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

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Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

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<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
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<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
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<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

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				20					25					30
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
				35					40					45
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
				50					55					60
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
				65					70					75
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
				80					85					90
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
				95					100					105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

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tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
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 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
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 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagttaa ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5				10						15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25						30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55						60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65				70						75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80				85						90



Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala	95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp	110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly	125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn	140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile	155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala	170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu	185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr	200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys	215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys	230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys	245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu	260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn	275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn	290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe	305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu	320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp	335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val	350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg			365	370	

<210> 367

<211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-30  
 <223> Synthetic construct.  
  
 <400> 367  
 tggaaaagaa gtctggtcag aaggtttagg 30  
  
 <210> 368  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.  
  
 <400> 368  
 catttggtt cattctcctg ctctg 25  
  
 <210> 369  
 <211> 28  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.  
  
 <400> 369  
 aaaacctcag aacaactcat ttgcacc 28  
  
 <210> 370  
 <211> 41  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-41  
 <223> Synthetic construct.  
  
 <400> 370  
 gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41  
  
 <210> 371  
 <211> 1150  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 371  
 gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
 ctggggcaac ccggtgctc ctgctcttgc tgatggcggt agcagcgccc 150  
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
 tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300  
 tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcgga 350  
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
 gaagctggtg gctatgtctc ctcttttgc cctgcgtgct ccctggtgga 500  
 gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600  
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
 gccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgcctgg 700  
 agatggaaca ggcccagaag gccagaacc ccagagagca gaagtccttc 750  
 ttgcgcaaat actggatgta catcattccc gtcgtcctgt tctcatgat 800  
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
 agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000  
 tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaaaccga gccggagccg gagccacagc ggggaggggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150

tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250  
 ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300  
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350  
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400  
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450  
 cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500  
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550  
 ctgctcttct cagccttcga ggcttggtat atccatgagc acgtggaacg 600  
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650  
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700  
 gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750  
 tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800  
 atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850  
 ctctgtcgg accgccgctg gctgctgctg ggcaccatac aagctctatt 900  
 tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950  
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000  
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050  
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100  
 tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150  
 tccttcatag cttttctact tattgagttg gcttgtggat tatactttcc 1200  
 cagcatgagc ttcttacgga gaaagtgat ccctgagaca gagcaggctg 1250  
 gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300  
 ctcttgttcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350  
 cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400  
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450  
 gaggagccct atgcccctga gctgtaaccc cactccagga caagatagct 1500  
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550  
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600  
 gggaggacat gatgggggtg atggactgga aagaagggtc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac acttttaa at gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser	
1				5					10					15	
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly	
				20					25					30	
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe	
				35					40					45	
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala	
				50					55					60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly	
				65					70					75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu	
				80					85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys	
				95					100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu	
				110					115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala	
				125					130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala	
				140					145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu	
				155					160					165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val	
				170					175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp	
				185					190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu	
				200					205					210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50

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gctccccgcg tgcgtcgccg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200

cctgccaaagg actttggtgg tatctttcac acaaggatatg agcagattca 250

ccttggtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 ttttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggatgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca ggcacagct gacatccccg ccctcttcct gctcggccga 500  
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atccagtc aatgtaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtcca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750  
 tttgggcggt gctaggctga aagggagcc acaccactgg ccttcccttc 800  
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccaggggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccaggggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
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Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90



Glu	Arg	Gly	Gly	Cys	Ser	Phe	Leu	Ser	Lys	Thr	Arg	Val	Val	Gln
				95					100					105
Glu	His	Gly	Gly	Arg	Ala	Val	Ile	Ile	Ser	Asp	Asn	Ala	Val	Asp
				110					115					120
Asn	Asp	Ser	Phe	Tyr	Val	Glu	Met	Ile	Gln	Asp	Ser	Thr	Gln	Arg
				125					130					135
Thr	Ala	Asp	Ile	Pro	Ala	Leu	Phe	Leu	Leu	Gly	Arg	Asp	Gly	Tyr
				140					145					150
Met	Ile	Arg	Arg	Ser	Leu	Glu	Gln	His	Gly	Leu	Pro	Trp	Ala	Ile
				155					160					165
Ile	Ser	Ile	Pro	Val	Asn	Val	Thr	Ser	Ile	Pro	Thr	Phe	Glu	Leu
				170					175					180
Leu	Gln	Pro	Pro	Trp	Thr	Phe	Trp							
				185										

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagaccacagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccag agagtataaa 50  
ggcgaatgtg aggggtgccg gcacaaccag acgccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggtgctc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccagggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatatggc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccaaagagg 500  
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ccagtaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
ggatatgggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
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Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
			20						25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
			35						40					45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	
				50					55					60	
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	
				65					70					75	
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	
				80					85					90	
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	
				95					100					105	
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	
				110					115					120	
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	
				125					130					135	
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	
				140					145					150	
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	
				155					160					165	
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			
				170					175						

<210> 384  
 <211> 2379  
 <212> DNA  
 <213> Homo sapiens

<400> 384  
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 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250  
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcctggg 400  
 tgtcagcgag ccctgactca ctacagtga gctgacagg gctgtcatgc 450  
 aactggcccc taagccaaag caaaagacct aaggacgacc ttgaacaat 500  
 acaaaggatg ggtttcaatg taattaggct actgagcggg tcagctgtag 550  
 cactggttat agccccact gtcttactga caatgctttc ttctgccgaa 600  
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700  
 gtttgtccct tcgtataac agccttcaaa aacttaagta taatcaattt 750  
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800  
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcatttctt 950  
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000  
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
 aacctggaac ttttgacctt gggatataac cggatccgaa gtttagccag 1100  
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
 cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250  
 gtcttgacc tggagctcct taaaaggct tgatttatca ggcaatgaga 1300  
 tcgaagcttt cagtggacc agtggtttcc agtgtgtccc gaatctgcag 1350  
 cgcctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400  
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
 aatgcagcag aaatatattgc tcccttgtaa actggctgaa aagttttaaa 1500  
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650  
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700  
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750  
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800  
 ctcgtcatcc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850  
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900  
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950  
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggctc caggagtggt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgcttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150  
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcac 2200  
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250  
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300  
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350  
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200					205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe
				215					220					225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys
				230					235					240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu
				245					250					255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly
				260					265					270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu
				275					280					285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser
				290					295					300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu
				305					310					315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe
				320					325					330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu
				335					340					345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile
				350					355					360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu
				365					370					375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu
				380					385					390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly
				395					400					405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile
				410					415					420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu
				425					430					435
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440					445					450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455					460					465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470					475					480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485					490					495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

gtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50

ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100

gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150

ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200



aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250  
 gcagctcttc tctgtggagc tgtggctctc tgcctccagt gctggctgag 300  
 gagaccccca attgattctc acaggcgcac catggcagtt tttgctgttg 350  
 gagacttgga ctctatztat gggacagaag cagctgtgag tccaactggt 400  
 ggaattcacc ttcaaaactca aaccctgac ctatatcctg ttcctgctcc 450  
 atgttttggc cctttaggct cccacacctc atatgaagaa attgtaaaaa 500  
 caacctgatt ttaggtgttg attatcaatt taaagtatta acgacatctg 550  
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600  
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650  
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gtaaagtagc 700  
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750  
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 tctgctttaa actctttcct agcatggggg ccataaaaaat tattataatt 900  
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 agatagttatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000  
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050  
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100  
 tntagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150  
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 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300  
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350  
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400  
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
			80						85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
			95						100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
			110						115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
			125						130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
			140						145						

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
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<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatgcagcaggaacagg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
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accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
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cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400  
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gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtgga tgtcgagaac ggtgcttcta 650  
tggcaggata tgccgatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750  
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ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900  
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aagctctaca catTTTcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100

aancagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150  
 aatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200  
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 taagagtatc ctttatgaaa ttttgaattt gtataacaga tgcattagat 1900  
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 tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000  
 accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050  
 atttccttg tagcaaatct aattgccaca tggtgcccta tatttcatag 2100  
 tatttattct ctatagtaac tgcttaagtg cagctagctt ctagatttag 2150  
 actatataga atttagatat tgtattgttc gtcattataa tatgctacca 2200  
 catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250  
 tttcatgaaa gacagatttc caaatctctc ttctcttctc tgtactgtct 2300  
 acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser

1

5

10

15

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                     20                    25                    30  
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
                     35                    40                    45  
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
                     50                    55                    60  
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
                     65                    70                    75  
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
                     80                    85                    90  
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
                     95                    100                    105  
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
                     110                    115                    120  
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
                     125                    130                    135  
 Ser Gly Ser Ile Arg  
                     140

<210> 396

<211> 2639

<212> DNA

<213> Homo sapiens

<400> 396

cgcgccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50  
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 gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150  
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
 cctgggcccc cacatcatgc cggtgcccac ccctctggac acagcccact 250  
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 gggccggggt acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
 caccagcacc tcacccactg ccttctcccc ccttcgctac ctggagtcgc 400  
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
 agctcaccac tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
 acctctccca caacctcatt caccgcctcg tgccccaccc caccgagggc 600  
 ggctgcctcg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700  
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 gccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850  
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 tcctgcagg agctggacct ttcgggcacc aacctggtgc ccctgcctga 950  
 ggcgtgtctc ctccacctcc cggcactgca gagegtcagc gtgggccagg 1000  
 atgtgcggtg ccggcgctg gtgcgggagg gcacctacc ccggaggcct 1050  
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 aggagtgtg ggcttaggag aggccttgga cctgggagcc acacctagga 1300  
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 gggcagaggg tgggtgggac cccctgctgc agggcagagt tcaggtccac 1500  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397  
<211> 353  
<212> PRT  
<213> Homo sapiens

<400> 397  
Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln  
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Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr  
20 25 30  
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser  
35 40 45  
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr  
50 55 60  
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu  
65 70 75  
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp  
80 85 90  
Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser  
95 100 105  
Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu  
110 115 120  
Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp  
125 130 135  
Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala  
140 145 150

Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
	155	160 165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
	170	175 180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
	185	190 195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
	200	205 210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
	215	220 225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
	230	235 240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
	245	250 255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
	260	265 270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
	275	280 285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
	290	295 300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
	305	310 315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
	320	325 330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
	335	340 345
Ala Ala Arg Gly	Pro Thr Ile Leu	
	350	

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA



<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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gtgggtctga ggggaccaga aggggtgagct acgttggtt tctggaagg 100  
gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150  
atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200  
ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250  
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300  
ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350  
tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400  
ctgcgtttta tctctatgg actccttcca ctggactgaa gacactcaat 450  
ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500  
ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550  
gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600  
tgctgcctcc tgcgccattt gctaagactc tatctggaca gggtatTTaa 650  
aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800  
 gaggcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850  
 gggaaacaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
 acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt 1000  
 cttgtgctgg tcacagtga tcttatttat gcattacttg cttccttgca 1050  
 tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag 1100  
 atttttgtaa tatctttctg ctattggata tatttatttag ttaatatatt 1150  
 tatttatctt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200  
 ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250  
 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
 ctaggggggt tattcatctg tattcaacta aggacatatt tactcatgct 1350  
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25					30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40					45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
cacccgccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatattgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttcttg 950  
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln  
1 5 10 15

Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

&lt;210&gt; 407

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-31

&lt;223&gt; Synthetic construct.

&lt;400&gt; 407

cgcgatccc gttatcgtct tgcgctactg c 31

&lt;210&gt; 408

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;221&gt; Artificial Sequence

&lt;222&gt; 1-34

&lt;223&gt; Synthetic construct.

&lt;400&gt; 408

gcggaattct taaaatggac tgactccact catc 34

&lt;210&gt; 409

&lt;211&gt; 1487

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaätg gcaggcttcc 150

tagataattt tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgtcgcäggg atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400

ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450

tgatgttttg gtcacttatt gcttccatgt ggattctttt tgggtgcatat 500

gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600  
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 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700  
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750  
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 ttgagggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050  
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 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250  
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300  
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350  
 ttttttggt aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400  
 tttatataat gattttttta atgccc aaag gactagtttg aaagcttctt 1450  
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410  
 <211> 158  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys  
 1 5 10 15  
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala  
 20 25 30  
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala  
 35 40 45  
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr  
 50 55 60  
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val  
 65 70 75

Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 411  
 gtttgaggaa gctgggatac 20

<210> 412  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 412  
 ccaaactcga gcacctgttc 20

<210> 413  
 <211> 40  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-40  
 <223> Synthetic construct.

<400> 413  
 atggcaggct tcctagataa ttttcggttg ccagaatgtg 40

<210> 414



<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414  
gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100  
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ctttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccctaa gccacccttc 300  
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350  
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450  
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500  
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
tactatgtgc tttgaagacc gcatgatcat gaggcctgtg aaaaacaatg 600  
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650  
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700  
gaaattcctt aaagaaattc cggggggtgc actggtgctg gtggcctcct 750  
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800  
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttaggggt gctgtggctc 1000  
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050  
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100  
gcaggctcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300  
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21  
 <223> Synthetic construct.  
  
 <400> 416  
 gccatagtca cgacatggat g 21  
  
 <210> 417  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 417  
 ggatggccag agctgctg 18  
  
 <210> 418  
 <211> 26  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.  
  
 <400> 418  
 aaagtacaag tgtggcctca tcaagc 26  
  
 <210> 419  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 419  
 tctgactcct aagtcaggca ggag 24  
  
 <210> 420  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 420  
 attctctcca cagacagctg gttc 24

<210> 421  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 421  
gtacaagtgt gccctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
<211> 1701  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1528  
<223> unknown base

<400> 422  
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150  
cacgccagga gtcgctcgc tctctctctc tctctctcac tectccctcc 200  
ctctctctct gctgtccta gtctcttagt cctcaaattc ccagtccct 250  
gcacccttc ctgggacact atgttggtct ccgccctcct gctggaggtg 300  
at ttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggcc 350  
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550  
tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg 600  
cactggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650  
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800  
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900  
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggtg 1050  
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100  
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc 1200  
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
ccttcccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450  
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550  
gaagtttggg atatacccca aagtctctta cccctcact tttatggccc 1600  
tttccctaga tatactgcgg gatctctcct taggataaag agttgctggt 1650  
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
1 5 10 15  
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80					85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala
				95					100					105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly
				110					115					120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His
				125					130					135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala
				140					145					150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu
				155					160					165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His
				170					175					180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro
				185					190					195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe
				200					205					210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val
				215					220					225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln
				230					235					240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro
				245					250					255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn
				260					265					270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr
				275					280					285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly
				290					295					300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile
				305					310					315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser
				320					325					330
Ala	Gln	Ala	Thr	Thr	Glu	Ala								
				335										

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 424  
 gtaaagtcgc tggccagc 18  
  
 <210> 425  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.  
  
 <400> 425  
 cccgatctgc ctgctgta 18  
  
 <210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.  
  
 <400> 426  
 ctgcactgta tggccattat tgtg 24  
  
 <210> 427  
 <211> 45  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.  
  
 <400> 427  
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45  
  
 <210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens  
  
 <400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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aacctgcttt gggactccct ccacaaaaac tggctccgga tcaggaaca 200
ctacaaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatc 300
ctgctgcagg aatgacacct ggtaccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcattctg 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc 600
gcctcccaac tccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
tatgtgcctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

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<210> 429
<211> 209
<212> PRT
<213> Homo sapiens

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<400> 429
Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1           5           10          15
Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
          20          25          30
Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
          35          40          45
Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
          50          55          60
Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
          65          70          75

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Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ggagagaggc ggcgcgggtga aaggcgcatt gatgcagcct gcgcgcgcct 50
cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgccgc ctccccgcag cggctccgcg gcctcctgct gtcctgctg 200
ctgcagctgc ccgcgccgtc gagcgccctt gagatcccca aggggaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaagatg cggtcaaata gtgctctaag 550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

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attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700  
 aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
 gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
 ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
 tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
 ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
 gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
 tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
 aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
 acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
 ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
 aatttgtaaa tgtaagaat tttttttata tctgttaaat aaaaattatt 1250  
 tccaaca 1257

<210> 431  
 <211> 243  
 <212> PRT  
 <213> Homo Sapien

<400> 431  
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
 1 5 10 15  
 Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 432  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial Sequence

<400> 432  
 aggacttgcc ctcaggaa 18

<210> 433  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 cgcaggacag ttgtgaaaat a 21

<210> 434  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 435  
 cccaactgta ccaccatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccactgtgtc tccc 24  
  
 <210> 437  
 <211> 19  
 <212> DNA  
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